

<110> Dean, Nicholas M.  
 Marcusson, Eric G.  
 Wyatt, Jacqueline  
 Zhang, Hong

<130> ISPH-545

<141>

<151> 2000-09-18

<151> 1999-04-12

&lt;170&gt; PatentIn Ver. 2.0

<213> Homo sapiens

<222> (221) . . (1228)

<309> 1996-07-19

5

20

25										30										35																				
agg aag act gtt act aca gtt gag act cag aac ttg gaa ggc ctg cat	Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn Leu Glu Gly Leu His	379																																						
40										45										50																				
cat gat ggc caa ttc tgc cat aag ccc tgt cct cca ggt gaa agg aaa	His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly Glu Arg Lys	427																																						
55										60										65																				
gct agg gac tgc aca gtc aat ggg gat gaa cca gac tgc gtg ccc tgc	Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val Pro Cys	475																																						
70										75										80										85										
caa gaa ggg aag gag tac aca gac aaa gcc cat ttt tct tcc aaa tgc	Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser Lys Cys	523																																						
90										95										100																				
aga aga tgt aga ttg tgt gat gaa gga cat ggc tta gaa gtg gaa ata	Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly Leu Glu Val Glu Ile	571																																						
105										110										115																				
aac tgc acc cgg acc cag aat acc aag tgc aga tgt aaa cca aac ttt	Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro Asn Phe	619																																						
120										125										130																				
ttt tgt aac tct act gta tgt gaa cac tgt gac cct tgc acc aaa tgt	Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr Lys Cys	667																																						
135										140										145																				
gaa cat gga atc atc aag gaa tgc aca ctc acc agc aac acc aag tgc	Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr Ser Asn Thr Lys Cys	715																																						
150										155										160										165										
aaa gag gaa gga tcc aga tct aac ttg ggg tgg ctt tgt ctt ctt ctt	Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp Leu Cys Leu Leu Leu	763																																						
170										175										180																				
ttg cca att cca cta att gtt tgg gtg aag aga aag gaa gta cag aaa	Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val Gln Lys	811																																						
185										190										195																				
aca tgc aga aag cac aga aag gaa aac caa ggt tct cat gaa tct cca	Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser His Glu Ser Pro	859																																						
200										205										210																				
acc tta aat cct gaa aca gtg gca ata aat tta tct gat gtt gac ttg	Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu Ser Asp Val Asp Leu	907																																						
215										220										225																				
agt aaa tat atc acc act att gct gga gtc atg aca cta agt caa gtt	Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr Leu Ser Gln Val	955																																						
230										235										240										245										
aaa ggc ttt gtt cga aag aat ggt gtc aat gaa gcc aaa ata gat gag	Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu	1003																																						
250										255										260																				
atc aag aat gac aat gtc caa gac aca gca gaa cag aaa gtt caa ctg	Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu	1051																																						

265	270	275	
ctt cgt aat tgg cat caa ctt cat	gga aag aaa gaa gcg tat gac aca	1099	
Leu Arg Asn Trp His Gln Leu His	Gly Lys Lys Glu Ala Tyr Asp Thr		
280	285	290	
ttg att aaa gat ctg aaa aaa gcc	aat ctt tgt act ctt gca gag aaa	1147	
Leu Ile Lys Asp Leu Lys Lys Ala	Asn Leu Cys Thr Leu Ala Glu Lys		
295	300	305	
att cag act atc atc ctc aag gac att	aet agt gac tca gaa aat tca	1195	
Ile Gln Thr Ile Ile Leu Lys Asp Ile	Thr Ser Asp Ser Glu Asn Ser		
310	315	320	325
aac ttc aga aat gaa atc caa agc ttg	gtc tag agtgaaaaac aacaaattca	1248	
Asn Phe Arg Asn Glu Ile Gln Ser Leu	Val		
330	335		
gttctgagta tatgcaatta gtgtttgaaa agattcttaa tagctggctg taaatactgc 1308			
ttggtttttt actgggtaca ttttatcatt tattagcgct gaagagccaa catatttgta 1368			
gatttttaaat atctcatgat tctgcctcca aggatgttta aaatctagtt gggaaaaacaa 1428			
acttcatcaa gagtaaatgc agtggcatgc taagtaccca aataggagtg tatgcagagg 1488			
atgaaagatt aagattatgc tctggcatct aacatatgat tctgtagtat gaatgtaatc 1548			
agtgtatggt agtacaaatg tctatccaca ggctaacccc actctatgaa tcaatagaag 1608			
aagctatgac cttttgctga aatatcagtt actgaacagg caggccactt tgcctctaaa 1668			
ttacctctga taattctaga gattttacca tattttctaaa ctttgtttat aactctgaga 1728			
agatcatatt tatgtaaagt atatgtatgt gagtgcagaa tttaaataag gctctacctc 1788			
aaagaccttt gcacagttta ttggtgtcat attatacaat atttcaattg tgaattcaca 1848			
tagaaaacat taaattataa tgtttgacta ttatatatgt gtatgcattt tactggctca 1908			
aaactaccta cttctttctc aggcatacaa agcattttga gcaggagagt attactagag 1968			
ctttgccacc tctccatttt tgccttggtg ctcatcttaa tggcctaattg ccccccaaa 2028			
catggaaata tcaccaaaaa atacttaata gtccacaaaa aggcaagact gcccttagaa 2088			
attctagcct ggtttgagaga tactaactgc tctcagagaa agtagctttg tgacatgtca 2148			
tgaacccatg tttgcaatca aagatgataa aatagattct tatttttccc ccacccccga 2208			
aaatgttcaa taatgtccca tgtaaaacct gctacaaatg gcagcttata catagcaatg 2268			
gtaaaatcat catctggatt taggaattgc tcttgtcata cccccaagtt tctaagattt 2328			
aagattctcc ttactactat cctacgttta aatatctttg aaagtttgta ttaaattgtga 2388			
attttaagaa ataataattta tattttctgta aatgtaaaact gtgaagatag ttataaactg 2448			
aagcagatac ctggaaccac ctaaagaact tccatttatg gaggattttt ttgcccttg 2508			

tgtttggaat tataaaatat aggtaaaagt acgtaattaa ata

2551

<210> 2

<211> 335

<212> PRT

<213> Homo sapiens-

<400> 2

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala  
1 5 10 15  
Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser  
20 25 30  
Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn  
35 40 45  
Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
50 55 60  
Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
65 70 75 80  
Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
85 90 95  
Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly  
100 105 110  
Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg  
115 120 125  
Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp  
130 135 140  
Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr  
145 150 155 160  
Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp  
165 170 175  
Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg  
180 185 190  
Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly  
195 200 205  
Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu  
210 215 220  
Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met  
225 230 235 240  
Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu  
245 250 255  
Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu  
260 265 270  
i

Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys  
275 280 285

Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys  
290 295 300

Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser  
305 310 315 320

Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val  
325 330 335

<210> 3  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence

<400> 3  
cgtaaaccgc ttccctcact 20

<210> 4  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence

<400> 4  
gtgttccgtg ccagtgcccg 20

<210> 5  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence

<400> 5  
gcccagcatg gttgttgagc 20

<210> 6  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence

<400> 6  
cttctcfaat tccaatccct 20

<210> 7

<211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 7  
 cttcttggca gggcacgcag 20  
  
 <210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 8  
 tgcacttggt attctgggtc 20  
  
 <210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 9  
 gctggtgagt gtgcattcct 20  
  
 <210> 10  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 10  
 cattgacacc attctttcga 20  
  
 <210> 11  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 11  
 tcactctaga ccaagctttg 20  
  
 <210> 12

<211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 12  
 cccagtaaaa aaccaagcag 20  
  
 <210> 13  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 13  
 tatgttggt cttcagcgct 20  
  
 <210> 14  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
 <400> 14  
 atttgggtac ttagcatgcc 20  
  
 <210> 15  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 15  
 gggttagcct gtggatagac 20  
  
 <210> 16  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 16  
 caaagtggcc tgcctgttca 20  
  
 <210> 17  
 <211> 20

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 17  
 ttgagccagt aaaatgcata 20  
  
 <210> 18  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 18  
 tgagcaccaa ggcaaaaatg 20  
  
 <210> 19  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 19  
 tcttgccctt tggtggacta 20  
  
 <210> 20  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 20  
 agcaggtttt acatgggaca 20  
  
 <210> 21  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 21  
 ggtatgacaa gagcaattcc 20  
  
 <210> 22  
 <211> 20



<212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 22  
 ggtggttcca ggtatctgct 20

<210> 23  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 23  
 tataattcca aacacaaggg 20

<210> 24  
 <211> 1890  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (189)..(1034)

<300>  
 <303> Biochim. Biophys. Acta  
 <304> 204  
 <305> 2  
 <306> 468-474  
 <307> 1994-10-28  
 <308> D31822/Genbank  
 <309> 1999-02-08

<400> 24  
 aaacagagag agatagagaa agagaaagac agaggtgttt cccttagcta tggaaactct 60  
 ataagagaga tccagcttgc ctctcttga gcagtcagca acaggggtccc gtccttgaca 120  
 cctcagcctc tacaggactg agaagaagta aaaccgtttg ctggggctgg cctgactcac 180  
 cagctgcc atg cag cag ccc ttc aat tac cca tat ccc cag atc tac tgg 230  
 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp  
 1 5 10

gtg gac agc agt gcc agc tct ccc tgg gcc cct cca ggc aca gtt ctt 278  
 Val Asp Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu  
 15 20 25 30

ccc tgt cca acc tct gtg ccc aga agg cct ggt caa agg agg cca cca 326  
 Pro Cys Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro  
 35 40 45

cca cca ccg cca ccg cca cca cta cca cct ccg ccg ccg ccg cca cca 374  
 Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro

50	55	60	
ctg cct cca cta ccg ctg cca ccc ctg aag aag aga ggg aac cac agc			422
Leu Pro Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser			
65	70	75	
aca ggc ctg tgt ctc ctt gtg atg ttt ttc atg gtt ctg gtt gcc ttg			470
Thr Gly Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu			
80	85	90	
gta gga ttg ggc ctg ggg atg ttt cag ctc ttc cac cta cag aag gag			518
Val Gly Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu			
95	100	105	110
ctg gca gaa ctc cga gag tct acc agc cag atg cac aca gca tca tct			566
Leu Ala Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser			
115	120	125	
ttg gag aag caa ata ggc cac ccc agt cca ccc cct gaa aaa aag gag			614
Leu Glu Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu			
130	135	140	
ctg agg aaa gtg gcc cat tta aca ggc aag tcc aac tca agg tcc atg			662
Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met			
145	150	155	
cct ctg gaa tgg gaa gac acc tat gga att gtc ctg ctt tct gga gtg			710
Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val			
160	165	170	
aag tat aag aag ggt ggc ctt gtg atc aat gaa act ggg ctg tac ttt			758
Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe			
175	180	185	190
gta tat tcc aaa gta tac ttc cgg ggt caa tct tgc aac aac ctg ccc			806
Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro			
195	200	205	
ctg agc cac aag gtc tac atg agg aac tct aag tat ccc cag gat ctg			854
Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu			
210	215	220	
gtg atg atg gag ggg aag atg atg agc tac tgc act act ggg cag atg			902
Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met			
225	230	235	
tgg gcc cgc agc agc tac ctg ggg gca gtg ttc aat ctt acc agt gct			950
Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala			
240	245	250	
gat cat tta tat gtc aac gta tct gag ctc tct ctg gtc aat ttt gag			998
Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu			
255	260	265	270
gaa tot cag acg ttt ttc ggc tta tat aag ctc taa gagaagcact			1044
Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu			
275	280		
ttgggattct ttccattatg attctttgtt acaggcaccg agaatgttgt attcagtgag			1104

ggtcttctta catgcatttg aggtcaagta agaagacatg aaccaagtgg accttgagac 1164  
 cacaggggttc aaaatgtctg tagctcctca actcacctaa tgtttatgag ccagacaaat 1224  
 ggaggaatat gacggaagaa catagaactc tgggctgcca tgtgaagagg gagaagcatg 1284  
 aaaaagcagc taccaggtg ttctacactc atcttagtgc ctgagagtat ttaggcagat 1344  
 tgaaaaggac accttttaac tcacctctca aggtgggcct tgctacctca aggggggactg 1404  
 tctttcagat acatggttgt gacctgagga ttttaaggat ggaaaaggaa gactagaggc 1464  
 ttgcataata agctaaagag gctgaaagag gccaatgccc cactggcagc atcttcactt 1524  
 ctaaatgcat atcctgagcc atcggtgaaa ctaacagata agcaagagag atgttttggg 1584  
 gactcatttc attcctaaca cagcatgtgt atttccagtg ccaattgtag ggggtgtgtgt 1644  
 gtgtgtgtgt gtgtgtgtgt atgactaaag agagaatgta gatattgtga agtacatatt 1704  
 aggaaaatat gggttgcatt tgggtcaagat tttgaatgct tcctgacaat caactctaata 1764  
 agtgcttaaa aatcattgat tgtcagctac taatgatgtt ttcctataat ataataaata 1824  
 tttatgtaga tgtgcatttt tgtgaaatga aaacatgtaa taaaaagtat atgttaggat 1884  
 acaaat 1890

<210> 25  
 <211> 281  
 <212> PRT  
 <213> Homo sapiens

<400> 25  
 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp  
 1 5 10 15  
 Ser Ser Ala Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys  
 20 25 30  
 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro  
 35 40 45  
 Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro  
 50 55 60  
 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly  
 65 70 75 80  
 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly  
 85 90 95  
 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala  
 100 105 110  
 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu  
 115 120 125  
 Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg

130	135	140
Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu		
145	150	155 160
Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr		
	165	170 175
Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr		
	180	185 190
Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser		
	195	200 205
His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met		
	210	215 220
Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala		
	225	230 235 240
Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His		
	245	250 255
Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser		
	260	265 270
Gln Thr Phe Phe Gly Leu Tyr Lys Leu		
	275	280

<210> 26  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 26  
 ccatagctaa gggaaacacc 20

<210> 27  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 27  
 gccagcccca gcaaacggtt 20

<210> 28  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic Sequence  
 <400> 28  
 tgcattggcag ctggtgagtc 20  
  
 <210> 29  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 29  
 ggaagaactg tgcctggagg 20  
  
 <210> 30  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 30  
 tggcagcggg agtggaggca 20  
  
 <210> 31  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 31  
 gctgtgtgca tctggctggg 20  
  
 <210> 32  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 32  
 aatgggccac tttcctcagc 20  
  
 <210> 33  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Synthetic Sequence  
 <400> 33  
 gcaggttggt gcaagattga 20  
 <210> 34  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
 <400> 34  
 aagattgaac actgccccca 20  
 <210> 35  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
 <400> 35  
 aatcccaaag tgcttctctt 20  
 <210> 36  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
 <400> 36  
 ttctcgtgc ctgtaacaaa 20  
 <210> 37  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
 <400> 37  
 gctacagaca ttttgaaccc 20  
 <210> 38  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 38  
ccgtcatatt cctccatttg 20

<210> 39  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Synthetic Sequence

<400> 39  
ccctcttcac atggcagccc 20

<210> 40  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Synthetic Sequence

<400> 40  
ggtgtccttt tcaatctgcc 20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence  
<400> 41  
cagtccccct tgaggtagca 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence

<400> 42  
gtgaagatgc tgccagtggg 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence

<400> 43  
cccctacaat tggcactgga 20

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence

<400> 44  
tcttgaccaa atgcaaccca 20

<210> 45  
<211> 8119  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (64)..(7521)

<300>  
<303> FEBS Lett.  
<304> 337  
<305> 2  
<306> 200-206  
<307> 1994-01-10  
<308> D21209/Genbank  
<309> 1999-02-05

<400> 45  
cgctccctgca gccctcgccc ggcgctccag tagcaggacc cggctctcggg accagccggg 60

aat atg cac gtg tca cta gct gag gcc ctg gag gtt cgg ggt gga cca 108  
Met His Val Ser Leu Ala Glu Ala Leu Val Arg Gly Gly Pro  
1 5 10 15

ctt cag gag gaa gaa ata tgg gct gta tta aat caa agt gct gaa agt 156  
Leu Gln Glu Glu Glu Ile Trp Ala Val Leu Asn Gln Ser Ala Glu Ser  
20 25 30

ctc caa gaa tta ttc aga aaa gta agc cta gct gat cct gct gcc ctt 204  
Leu Gln Glu Leu Phe Arg Lys Val Ser Leu Ala Asp Pro Ala Ala Leu  
35 40 45

ggc ttc atc att tct cca tgg tct ctg ctg ttg ctg cca tct ggt agt 252  
Gly Phe Ile Ile Ser Pro Trp Ser Leu Leu Leu Pro Ser Gly Ser  
50 55 60

gtg tca ttt aca gat gaa aat att tcc aat cag gat ctt cga gca ttc 300  
Val Ser Phe Thr Asp Glu Asn Ile Ser Asn Gln Asp Leu Arg Ala Phe  
65 70 75

act gca cca gag gtt ctt caa aat cag tca cta act tct ctc tca gat 348  
Thr Ala Pro Glu Val Leu Gln Asn Gln Ser Leu Thr Ser Leu Ser Asp  
80 85 90 95



gtt gaa aag atc cac att tat tct ctt gga atg aca ctg tat tgg ggg	396
Val Glu Lys Ile His Ile Tyr Ser Leu Gly Met Thr Leu Tyr Trp Gly	
100 105 110	
gct gat tat gaa gtg cct cag agc caa cct att aag ctt gga gat cat	444
Ala Asp Tyr Glu Val Pro Gln Ser Gln Pro Ile Lys Leu Gly Asp His	
115 120 125	
ctc aac agc ata ctg ctt gga atg tgt gag gat gtt att tac gct cga	492
Leu Asn Ser Ile Leu Leu Gly Met Cys Glu Asp Val Ile Tyr Ala Arg	
130 135 140	
gtt tct gtt cgg act gtg ctg gat gct tgc agt gcc cac att agg aat	540
Val Ser Val Arg Thr Val Leu Asp Ala Cys Ser Ala His Ile Arg Asn	
145 150 155	
agc aat tgt gca ccc tca ttt tcc tac gtg aaa cac ttg gta aaa ctg	588
Ser Asn Cys Ala Pro Ser Phe Ser Tyr Val Lys His Leu Val Lys Leu	
160 165 170 175	
gtt ctg gga aat ctt tct ggg aca gat cag ctt tcc tgt aac agt gaa	636
Val Leu Gly Asn Leu Ser Gly Thr Asp Gln Leu Ser Cys Asn Ser Glu	
180 185 190	
caa aag cct gat cga agc cag gct att cga gat cga ttg cga gga aaa	684
Gln Lys Pro Asp Arg Ser Gln Ala Ile Arg Asp Arg Leu Arg Gly Lys	
195 200 205	
gga tta cca aca gga aga agc tct act tct gat gta cta gac ata caa	732
Gly Leu Pro Thr Gly Arg Ser Ser Thr Ser Asp Val Leu Asp Ile Gln	
210 215 220	
aag cct cca ctc tct cat cag acc ttt ctt aac aaa ggg ctt agt aaa	780
Lys Pro Pro Leu Ser His Gln Thr Phe Leu Asn Lys Gly Leu Ser Lys	
225 230 235	
tct atg gga ttt ctg tcc atc aaa gat aca caa gat gag aat tat ttc	828
Ser Met Gly Phe Leu Ser Ile Lys Asp Thr Gln Asp Glu Asn Tyr Phe	
240 245 250 255	
aag gac att tta tca gat aat tct gga cgt gaa gat tct gaa aat aca	876
Lys Asp Ile Leu Ser Asp Asn Ser Gly Arg Glu Asp Ser Glu Asn Thr	
260 265 270	
ttc tcc cct tac cag ttc aaa act agt ggc cca gaa aaa aaa ccc atc	924
Phe Ser Pro Tyr Gln Phe Lys Thr Ser Gly Pro Glu Lys Lys Pro Ile	
275 280 285	
cct ggc att gat gtg ctt tct aag aag aag atc tgg gct tca tcc atg	972
Pro Gly Ile Asp Val Leu Ser Lys Lys Lys Ile Trp Ala Ser Ser Met	
290 295 300	
gac ttg ctt tgt aca gct gac aga gac ttc tct tca gga gag act gcc	1020
Asp Leu Leu Cys Thr Ala Asp Arg Asp Phe Ser Ser Gly Glu Thr Ala	
305 310 315	
aca tat cgt cgt tgt cac cct gag gca gta aca gtg cgg act tca act	1068
Thr Tyr Arg Arg Cys His Pro Glu Ala Val Thr Val Arg Thr Ser Thr	
320 325 330 335	

act cct aga aaa aag gag gca aga tac tca gat gga agt ata gcc ttg	1116
Thr Pro Arg Lys Lys Glu Ala Arg Tyr Ser Asp Gly Ser Ile Ala Leu	
340 345 350	
gat atc ttt ggc cct cag aaa atg gat cca ata tat cac act cga gaa	1164
Asp Ile Phe Gly Pro Gln Lys Met Asp Pro Ile Tyr His Thr Arg Glu	
355 360 365	
ttg ccc acc tcc tca gca ata tca agt gct ttg gac cga atc cga gag	1212
Leu Pro Thr Ser Ser Ala Ile Ser Ser Ala Leu Asp Arg Ile Arg Glu	
370 375 380	
aga caa aag aaa ctt cag gtt ctg agg gaa gcc atg aat gta gaa gaa	1260
Arg Gln Lys Lys Leu Gln Val Leu Arg Glu Ala Met Asn Val Glu Glu	
385 390 395	
cca gtt cga aga tac aaa act tat cat ggt gat gtc ttt agt acc tcc	1308
Pro Val Arg Arg Tyr Lys Thr Tyr His Gly Asp Val Phe Ser Thr Ser	
400 405 410 415	
agt gaa agt cca tct att att tcc tct gaa tca gat ttc aga caa gtg	1356
Ser Glu Ser Pro Ser Ile Ile Ser Ser Glu Ser Asp Phe Arg Gln Val	
420 425 430	
aga aga agt gaa gcc tca aag agg ttt gaa tcc agc agt ggt ctc cca	1404
Arg Arg Ser Glu Ala Ser Lys Arg Phe Glu Ser Ser Ser Gly Leu Pro	
435 440 445	
ggg gta gat gaa acc tta agt caa ggc cag tca cag aga ccg agc aga	1452
Gly Val Asp Glu Thr Leu Ser Gln Gly Gln Ser Gln Arg Pro Ser Arg	
450 455 460	
caa tat gaa aca ccc ttt gaa ggc aac tta att aat caa gag atc atg	1500
Gln Tyr Glu Thr Pro Phe Glu Gly Asn Leu Ile Asn Gln Glu Ile Met	
465 470 475	
cta aaa cgg caa gag gaa gaa ctg atg cag cta caa gcc aaa atg gcc	1548
Leu Lys Arg Gln Glu Glu Glu Leu Met Gln Leu Gln Ala Lys Met Ala	
480 485 490 495	
ctt aga cag tct cgg ttg agc cta tat cca gga gac aca atc aaa gcg	1596
Leu Arg Gln Ser Arg Leu Ser Leu Tyr Pro Gly Asp Thr Ile Lys Ala	
500 505 510	
tcc atg ctt gac atc acc agg gat ccg tta aga gaa att gcc cta gaa	1644
Ser Met Leu Asp Ile Thr Arg Asp Pro Leu Arg Glu Ile Ala Leu Glu	
515 520 525	
aca gcc atg act caa aga aaa ctg agg aat ttc ttt ggc cct gag ttt	1692
Thr Ala Met Thr Gln Arg Lys Leu Arg Asn Phe Phe Gly Pro Glu Phe	
530 535 540	
gtg aaa atg aca att gaa cca ttt ata tct ttg gat ttg cca cgg tct	1740
Val Lys Met Thr Ile Glu Pro Phe Ile Ser Leu Asp Leu Pro Arg Ser	
545 550 555	
att ctt act aag aaa ggg aag aat gag gat aac cga agg aaa gta aac	1788
Ile Leu Thr Lys Lys Gly Lys Asn Glu Asp Asn Arg Arg Lys Val Asn	
560 565 570 575	

ata atg ctt ctg aac ggg caa aga ctg gaa ctg acc tgt gat acc aaa	1836
Ile Met Leu Leu Asn Gly Gln Arg Leu Glu Leu Thr Cys Asp Thr Lys	
580 585 590	
act ata tgt aaa gat gtg ttt gat atg gtt gtg gca cat att ggc tta	1884
Thr Ile Cys Lys Asp Val Phe Asp Met Val Val Ala His Ile Gly Leu	
595 600 605	
gta gag cat cat ttg ttt gct tta gct acc ctc aaa gat aat gaa tat	1932
Val Glu His Leu Phe Ala Leu Ala Thr Leu Lys Asp Asn Glu Tyr	
610 615 620	
ttc ttt gtt gat cct gac tta aaa tta acc aaa gtg gcc cca gag gga	1980
Phe Phe Val Asp Pro Asp Leu Lys Leu Thr Lys Val Ala Pro Glu Gly	
625 630 635	
tgg aaa gaa gaa cca aag aaa aag acc aaa gcc act gtt aat ttt act	2028
Trp Lys Glu Glu Pro Lys Lys Lys Thr Lys Ala Thr Val Asn Phe Thr	
640 645 650 655	
ttg ttt ttc aga att aaa ttt ttt atg gat gat gtt agt cta ata caa	2076
Leu Phe Phe Arg Ile Lys Phe Phe Met Asp Asp Val Ser Leu Ile Gln	
660 665 670	
cat act ctg acg tgt cat cag tat tac ctt cag ctt cga aaa gat att	2124
His Thr Leu Thr Cys His Gln Tyr Tyr Leu Gln Leu Arg Lys Asp Ile	
675 680 685	
ttg gag gaa agg atg cac tgt gat gat gag act tcc tta ttg ctg gca	2172
Leu Glu Glu Arg Met His Cys Asp Asp Glu Thr Ser Leu Leu Leu Ala	
690 695 700	
tcc ttg gct ctc cag gct gag tat gga gat tat caa cca gag gtt cat	2220
Ser Leu Ala Leu Gln Ala Glu Tyr Gly Asp Tyr Gln Pro Glu Val His	
705 710 715	
ggg gtg tct tac ttt aga atg gag cac tat ttg ccc gcc aga gtg atg	2268
Gly Val Ser Tyr Phe Arg Met Glu His Tyr Leu Pro Ala Arg Val Met	
720 725 730 735	
gag aaa ctt gat tta tcc tat atc aaa gaa gag tta ccc aaa ttg cat	2316
Glu Lys Leu Asp Leu Ser Tyr Ile Lys Glu Glu Leu Pro Lys Leu His	
740 745 750	
aat acc tat gtg gga gct tct gaa aaa gag aca gag tta gaa ttt tta	2364
Asn Thr Tyr Val Gly Ala Ser Glu Lys Glu Thr Glu Leu Glu Phe Leu	
755 760 765	
aag gtc tgc caa aga ctg aca gaa tat gga gtt cat ttt cac cga gtg	2412
Lys Val Cys Gln Arg Leu Thr Glu Tyr Gly Val His Phe His Arg Val	
770 775 780	
cac cct gag aag aag tca caa aca gga ata ttg ctt gga gtc tgt tct	2460
His Pro Glu Lys Lys Ser Gln Thr Gly Ile Leu Leu Gly Val Cys Ser	
785 790 795	
aaa ggt gtc ctt gtg ttt gaa gtt cac aat gga gtg cgc aca ttg gtc	2508
Lys Gly Val Leu Val Phe Glu Val His Asn Gly Val Arg Thr Leu Val	
800 805 810 815	

ctt cgc ttt cca tgg agg gaa acc aag aaa ata tct ttt tct aaa aag	2556
Leu Arg Phe Pro Trp Arg Glu Thr Lys Lys Ile Ser Phe Ser Lys Lys	
820 825 830	
aaa atc aca ttg caa aat aca tca gat gga ata aaa cat ggc ttc cag	2604
Lys Ile Thr Leu Gln Asn Thr Ser Asp Gly Ile Lys His Gly Phe Gln	
835 840 845	
aqa gac aac agt aag ata tgc cag tac ctg ctg cac ctc tgc tct tac	2652
Thr Asp Asn Ser Lys Ile Cys Gln Tyr Leu Leu His Leu Cys Ser Tyr	
850 855 860	
cag cat aag ttc cag cta cag atg aga gca aga cag agc aac caa gat	2700
Gln His Lys Phe Gln Leu Gln Met Arg Ala Arg Gln Ser Asn Gln Asp	
865 870 875	
gcc caa gat att gag aga gct tcg ttt agg agc ctg aat ctc caa gca	2748
Ala Gln Asp Ile Glu Arg Ala Ser Phe Arg Ser Leu Asn Leu Gln Ala	
880 885 890 895	
gag tct gtt aga gga ttt aat atg gga cga gca atc agc act ggc agt	2796
Glu Ser Val Arg Gly Phe Asn Met Gly Arg Ala Ile Ser Thr Gly Ser	
900 905 910	
ctg gcc agc agc acc ctc aac aaa ctt gct gtt cga cct tta tca gtt	2844
Leu Ala Ser Ser Thr Leu Asn Lys Leu Ala Val Arg Pro Leu Ser Val	
915 920 925	
caa gct gag att ctg aag agg cta tcc tgc tca gag ctg tcg ctt tac	2892
Gln Ala Glu Ile Leu Lys Arg Leu Ser Cys Ser Glu Leu Ser Leu Tyr	
930 935 940	
cag cca ttg caa aac agt tca aaa gag aag aat gac aaa gct tca tgg	2940
Gln Pro Leu Gln Asn Ser Ser Lys Glu Lys Asn Asp Lys Ala Ser Trp	
945 950 955	
gag gaa aag cct aga gag atg agt aaa tca tac cat gat ctc agt cag	2988
Glu Glu Lys Pro Arg Glu Met Ser Lys Ser Tyr His Asp Leu Ser Gln	
960 965 970 975	
gcc tct ctc tat cca cat cgg aaa aat gtc att gtt aac atg gaa ccc	3036
Ala Ser Leu Tyr Pro His Arg Lys Asn Val Ile Val Asn Met Glu Pro	
980 985 990	
cca cca caa acc gtt gca gag ttg gtg gga aaa cct tct cac cag atg	3084
Pro Pro Gln Thr Val Ala Glu Leu Val Gly Lys Pro Ser His Gln Met	
995 1000 1005	
tca aga tct gat gca gaa tct ttg gca gga gtg aca aaa ctt aat aat	3132
Ser Arg Ser Asp Ala Glu Ser Leu Ala Gly Val Thr Lys Leu Asn Asn	
1010 1015 1020	
tca aag tct gtt gcg agt tta aat aga agt cct gaa agg agg aaa cat	3180
Ser Lys Ser Val Ala Ser Leu Asn Arg Ser Pro Glu Arg Arg Lys His	
1025 1030 1035	
gaa tca gac tcc tca tcc att gaa gac cct ggg caa gca tat gtt cta	3228
Glu Ser Asp Ser Ser Ser Ile Glu Asp Pro Gly Gln Ala Tyr Val Leu	
1040 1045 1050 1055	

gga atg act atg cat agt tct gga aac tct tca tcc caa gta ccc tta	3276
Gly Met Thr Met His Ser Ser Gly Asn Ser Ser Ser Gln Val Pro Leu	
1060 1065 1070	
aaa gaa aat gat gtg cta cac aaa aga tgg agc ata gta tct tca cca	3324
Lys Glu Asn Asp Val Leu His Lys Arg Trp Ser Ile Val Ser Ser Pro	
1075 1080 1085	
gaa agg gag atc acc tta gtg aac ctg aaa aaa gat gca aag tat ggc	3372
Glu Arg Glu Ile Thr Leu Val Asn Leu Lys Lys Asp Ala Lys Tyr Gly	
1090 1095 1100	
ttg gga ttt caa att att ggt ggg gag aag atg gga aga ctg gac cta	3420
Leu Gly Phe Gln Ile Ile Gly Gly Glu Lys Met Gly Arg Leu Asp Leu	
1105 1110 1115	
ggc ata ttt atc agt tca gtt gcc cct gga gga cca gct gac ttg gat	3468
Gly Ile Phe Ile Ser Ser Val Ala Pro Gly Gly Pro Ala Asp Leu Asp	
1120 1125 1130 1135	
gga tgc ttg aag cca gga gac cgt ttg ata tct gtg aat agt gtg agt	3516
Gly Cys Leu Lys Pro Gly Asp Arg Leu Ile Ser Val Asn Ser Val Ser	
1140 1145 1150	
ctg gag gga gtc agc cac cat gct gca att gaa att ttg caa aat gca	3564
Leu Glu Gly Val Ser His His Ala Ala Ile Glu Ile Leu Gln Asn Ala	
1155 1160 1165	
cct gaa gat gtg aca ctt gtt atc tct cag cca aaa gaa aag ata tcc	3612
Pro Glu Asp Val Thr Leu Val Ile Ser Gln Pro Lys Glu Lys Ile Ser	
1170 1175 1180	
aaa gtg cct tct act cct gtg cat ctc acc aat gag atg aaa aac tac	3660
Lys Val Pro Ser Thr Pro Val His Leu Thr Asn Glu Met Lys Asn Tyr	
1185 1190 1195	
atg aag aaa tct tcc tac atg caa gac agt gct ata gat tct tct tcc	3708
Met Lys Lys Ser Ser Tyr Met Gln Asp Ser Ala Ile Asp Ser Ser Ser	
1200 1205 1210 1215	
aag gat cac cac tgg tca cgt ggt acc ctg agg cac atc tcg gag aac	3756
Lys Asp His His Trp Ser Arg Gly Thr Leu Arg His Ile Ser Glu Asn	
1220 1225 1230	
tcc ttt ggg cca tct ggg ggc ctg cgg gaa gga agc ctg agt tct caa	3804
Ser Phe Gly Pro Ser Gly Gly Leu Arg Glu Gly Ser Leu Ser Ser Gln	
1235 1240 1245	
gat tcc agg act gag agt gcc agc ttg tct caa agc cag gtc aat ggt	3852
Asp Ser Arg Thr Glu Ser Ala Ser Leu Ser Gln Ser Gln Val Asn Gly	
1250 1255 1260	
ttc ttt gcc agc cat tta ggt gac caa acc tgg cag gaa tca cag cat	3900
Phe Phe Ala Ser His Leu Gly Asp Gln Thr Trp Gln Glu Ser Gln His	
1265 1270 1275	
ggc agc cct tcc cca tct gta ata tcc aaa gcc acc gag aaa gag act	3948
Gly Ser Pro Ser Pro Ser Val Ile Ser Lys Ala Thr Glu Lys Glu Thr	
1280 1285 1290 1295	

ttc act gat agt aac caa agc aaa act aaa aag cca ggc att tct gat	3996
Phe Thr Asp Ser Asn Gln Ser Lys Thr Lys Lys Pro Gly Ile Ser Asp	
1300 1305 1310	
gta act gat tac tca gac cgt gga gat tca gac atg gat gaa gcc act	4044
Val Thr Asp Tyr Ser Asp Arg Gly Asp Ser Asp Met Asp Glu Ala Thr	
1315 1320 1325	
tac tcc agc agt cag gat cat caa aca cca aaa cag gaa tct tcc tct	4092
Tyr Ser Ser Ser Gln Asp His Gln Thr Pro Lys Gln Glu Ser Ser Ser	
1330 1335 1340	
tca gtg aat aca tcc aac aag atg aat ttt aaa act ttt tct tca tca	4140
Ser Val Asn Thr Ser Asn Lys Met Asn Phe Lys Thr Phe Ser Ser Ser	
1345 1350 1355	
cct cct aag cct gga gat atc ttt gag gtt gaa ctg gct aaa aat gat	4188
Pro Pro Lys Pro Gly Asp Ile Phe Glu Val Glu Leu Ala Lys Asn Asp	
1360 1365 1370 1375	
aac agc ttg ggg ata agt gtc acg gga ggt gtg aat acg agt gtc aga	4236
Asn Ser Leu Gly Ile Ser Val Thr Gly Gly Val Asn Thr Ser Val Arg	
1380 1385 1390	
cat ggt ggc att tat gtg aaa gct gtt att ccc cag gga gca gca gag	4284
His Gly Gly Ile Tyr Val Lys Ala Val Ile Pro Gln Gly Ala Ala Glu	
1395 1400 1405	
tct gat ggt aga att cac aaa ggt gat cgc gtc cta gct gtc aat gga	4332
Ser Asp Gly Arg Ile His Lys Gly Asp Arg Val Leu Ala Val Asn Gly	
1410 1415 1420	
gtt agt cta gaa gga gcc acc cat aag caa gct gtg gaa aca ctg aga	4380
Val Ser Leu Glu Gly Ala Thr His Lys Gln Ala Val Glu Thr Leu Arg	
1425 1430 1435	
aat aca gga cag gtg gtt cat ctg tta tta gaa aag gga caa tct cca	4428
Asn Thr Gly Gln Val Val His Leu Leu Leu Glu Lys Gly Gln Ser Pro	
1440 1445 1450 1455	
aca tct aaa gaa cat gtc ccg gta acc cca cag tgt acc ctt tca gat	4476
Thr Ser Lys Glu His Val Pro Val Thr Pro Gln Cys Thr Leu Ser Asp	
1460 1465 1470	
cag aat gcc caa ggt caa ggc cca gaa aaa gtg aag aaa aca act cag	4524
Gln Asn Ala Gln Gly Gln Gly Pro Glu Lys Val Lys Lys Thr Thr Gln	
1475 1480 1485	
gtc aaa gac tac agc ttt gtc act gaa gaa aat aca ttt gag gta aaa	4572
Val Lys Asp Tyr Ser Phe Val Thr Glu Glu Asn Thr Phe Glu Val Lys	
1490 1495 1500	
tta ttt aaa aat agc tca ggt cta gga ttc agt ttt tct cga gaa gat	4620
Leu Phe Lys Asn Ser Ser Gly Leu Gly Phe Ser Phe Ser Arg Glu Asp	
1505 1510 1515	
aat ctt ata ccg gag caa att aat gcc agc ata gta agg gtt aaa aag	4668
Asn Leu Ile Pro Glu Gln Ile Asn Ala Ser Ile Val Arg Val Lys Lys	
1520 1525 1530 1535	

ctc ttt cct gga cag cca gca gca gaa agt gga aaa att gat gta gga	4716
Leu Phe Pro Gly Gln Pro Ala Ala Glu Ser Gly Lys Ile Asp Val Gly	
1540 1545 1550	
gat gtt atc ttg aaa gtg aat gga gcc tct ttg aaa gga cta tct cag	4764
Asp Val Ile Leu Lys Val Asn Gly Ala Ser Leu Lys Gly Leu Ser Gln	
1555 1560 1565	
cag gaa gtc ata tct gct ctc agg gga act gct cca gaa gta ttc ttg	4812
Gln Glu Val Ile Ser Ala Leu Arg Gly Thr Ala Pro Glu Val Phe Leu	
1570 1575 1580	
ctt ctc tgc aga cct cca cct ggt gtg cta ccg gaa att gat act gcg	4860
Leu Leu Cys Arg Pro Pro Pro Gly Val Leu Pro Glu Ile Asp Thr Ala	
1585 1590 1595	
ctt ttg acc cca ctt cag tct cca gca caa gta ctt cca aac agc agt	4908
Leu Leu Thr Pro Leu Gln Ser Pro Ala Gln Val Leu Pro Asn Ser Ser	
1600 1605 1610 1615	
aaa gac tct tct cag cca tca tgt gtg gag caa agc acc agc tca gat	4956
Lys Asp Ser Ser Gln Pro Ser Cys Val Glu Gln Ser Thr Ser Ser Asp	
1620 1625 1630	
gaa aat gaa atg tca gac aaa agc aaa aaa cag tgc aag tcc cca tcc	5004
Glu Asn Glu Met Ser Asp Lys Ser Lys Lys Gln Cys Lys Ser Pro Ser	
1635 1640 1645	
aga aga gac agt tac agt gac agc agt ggg agt gga gaa gat gac tta	5052
Arg Arg Asp Ser Tyr Ser Asp Ser Ser Gly Ser Gly Glu Asp Asp Leu	
1650 1655 1660	
gtg aca gct cca gca aac ata tca aat tcg acc tgg agt tca gct ttg	5100
Val Thr Ala Pro Ala Asn Ile Ser Asn Ser Thr Trp Ser Ser Ala Leu	
1665 1670 1675	
cat cag act cta agc aac atg gta tca cag gca cag agt cat cat gaa	5148
His Gln Thr Leu Ser Asn Met Val Ser Gln Ala Gln Ser His His Glu	
1680 1685 1690 1695	
gca ccc aag agt caa gaa gat acc att tgt acc atg ttt tac tat cct	5196
Ala Pro Lys Ser Gln Glu Asp Thr Ile Cys Thr Met Phe Tyr Tyr Pro	
1700 1705 1710	
cag aaa att ccc aat aaa cca gag ttt gag gac agt aat cct tcc cct	5244
Gln Lys Ile Pro Asn Lys Pro Glu Phe Glu Asp Ser Asn Pro Ser Pro	
1715 1720 1725	
cta cca ccg gat atg gct cct ggg cag agt tat caa ccc caa tca gaa	5292
Leu Pro Pro Asp Met Ala Pro Gly Gln Ser Tyr Gln Pro Gln Ser Glu	
1730 1735 1740	
tct gct tcc tct agt tcg atg gat aag tat cat ata cat cac att tct	5340
Ser Ala Ser Ser Ser Met Asp Lys Tyr His Ile His His Ile Ser	
1745 1750 1755	
gaa cca act aga caa gaa aac tgg aca cct ttg aaa aat gac ttg gaa	5388
Glu Pro Thr Arg Gln Glu Asn Trp Thr Pro Leu Lys Asn Asp Leu Glu	
1760 1765 1770 1775	

aat cac ctt gaa gac ttt gaa ctg gaa gta gaa ctc ctc att acc cta	5436
Asn His Leu Glu Asp Phe Glu Leu Glu Val Glu Leu Leu Ile Thr Leu	
1780 1785 1790	
att aaa tca gaa aaa gga agc ctg ggt ttt aca gta acc aaa ggc aat	5484
Ile Lys Ser Glu Lys Gly Ser Leu Gly Phe Thr Val Thr Lys Gly Asn	
1795 1800 1805	
cag aga att ggt tgt tat gtt cat gat gtc ata cag gat cca gcc aaa	5532
Gln Arg Ile Gly Cys Tyr Val His Asp Val Ile Gln Asp Pro Ala Lys	
1810 1815 1820	
agt gat gga agg cta aaa cct ggg gac cgg ctc ata aag gtt aat gat	5580
Ser Asp Gly Arg Leu Lys Pro Gly Asp Arg Leu Ile Lys Val Asn Asp	
1825 1830 1835	
aca gat gtt act aat atg act cat aca gat gca gtt aat ctg ctc cgg	5628
Thr Asp Val Thr Asn Met Thr His Thr Asp Ala Val Asn Leu Leu Arg	
1840 1845 1850 1855	
gct gca tcc aaa aca gtc aga tta gtt att gga cga gtt cta gaa tta	5676
Ala Ala Ser Lys Thr Val Arg Leu Val Ile Gly Arg Val Leu Glu Leu	
1860 1865 1870	
ccc aga ata cca atg ttg cct cat ttg cta ccg gac ata aca cta acg	5724
Pro Arg Ile Pro Met Leu Pro His Leu Leu Pro Asp Ile Thr Leu Thr	
1875 1880 1885	
tgc aac aaa gag gag ttg ggt ttt tcc tta tgt gga ggt cat gac agc	5772
Cys Asn Lys Glu Glu Leu Gly Phe Ser Leu Cys Gly Gly His Asp Ser	
1890 1895 1900	
ctt tat caa gtg gta tat att agt gat att aat cca agg tcc gtc gca	5820
Leu Tyr Gln Val Val Tyr Ile Ser Asp Ile Asn Pro Arg Ser Val Ala	
1905 1910 1915	
gcc att gag ggt aat ctc cag cta tta gat gtc atc cat tat gtg aac	5868
Ala Ile Glu Gly Asn Leu Gln Leu Leu Asp Val Ile His Tyr Val Asn	
1920 1925 1930 1935	
gga gtc agc aca caa gga atg acc ttg gag gaa gtt aac aga gca tta	5916
Gly Val Ser Thr Gln Gly Met Thr Leu Glu Glu Val Asn Arg Ala Leu	
1940 1945 1950	
gac atg tca ctt cct tca ttg gta ttg aaa gca aca aga aat gat ctt	5964
Asp Met Ser Leu Pro Ser Leu Val Leu Lys Ala Thr Arg Asn Asp Leu	
1955 1960 1965	
cca gtg gtc ccc agc tca aag agg tct gct gtt tca gct cca aag tca	6012
Pro Val Val Pro Ser Ser Lys Arg Ser Ala Val Ser Ala Pro Lys Ser	
1970 1975 1980	
acc aaa ggc aat ggt tcc tac agt gtg ggg tct tgc agc cag cct gcc	6060
Thr Lys Gly Asn Gly Ser Tyr Ser Val Gly Ser Cys Ser Gln Pro Ala	
1985 1990 1995	
ctc act cct aat gat tca ttc tcc acg gtt gct ggg gaa gaa ata aat	6108
Leu Thr Pro Asn Asp Ser Phe Ser Thr Val Ala Gly Glu Glu Ile Asn	
2000 2005 2010 2015	



gaa ata tcg tac ccc aaa gga aaa tgt tct act tat cag ata aag gga	6156
Glu Ile Ser Tyr Pro Lys Gly Lys Cys Ser Thr Tyr Gln Ile Lys Gly	
2020 2025 2030	
tca cca aac ttg act ctg ccc aaa gaa tct tat ata caa gaa gat gac	6204
Ser Pro Asn Leu Thr Leu Pro Lys Glu Ser Tyr Ile Gln Glu Asp Asp	
2035 2040 2045	
att tat gat gat tcc caa gaa gct gaa gtt atc cag tct ctg ctg gat	6252
Ile Tyr Asp Asp Ser Gln Glu Ala Glu Val Ile Gln Ser Leu Leu Asp	
2050 2055 2060	
gtt gtg gat gag gaa gcc cag aat ctt tta aac gaa aat aat gca gca	6300
Val Val Asp Glu Glu Ala Gln Asn Leu Leu Asn Glu Asn Asn Ala Ala	
2065 2070 2075	
gga tac tcc tgt ggt cca ggt aca tta aag atg aat ggg aag tta tca	6348
Gly Tyr Ser Cys Gly Pro Gly Thr Leu Lys Met Asn Gly Lys Leu Ser	
2080 2085 2090 2095	
gaa gag aga aca gaa gat aca gac tgc gat ggt tca cct tta cct gag	6396
Glu Glu Arg Thr Glu Asp Thr Asp Cys Asp Gly Ser Pro Leu Pro Glu	
2100 2105 2110	
tat ttt act gag gcc acc aaa atg aat ggc tgt gaa gaa tat tgt gaa	6444
Tyr Phe Thr Glu Ala Thr Lys Met Asn Gly Cys Glu Glu Tyr Cys Glu	
2115 2120 2125	
gaa aaa gta aaa agt gaa agc tta att cag aag cca caa gaa aag aag	6492
Glu Lys Val Lys Ser Glu Ser Leu Ile Gln Lys Pro Gln Glu Lys Lys	
2130 2135 2140	
act gat gat gat gaa ata aca tgg gga aat gat gag ttg cca ata gag	6540
Thr Asp Asp Asp Glu Ile Thr Trp Gly Asn Asp Glu Leu Pro Ile Glu	
2145 2150 2155	
aga aca aac cat gaa gat tct gat aaa gat cat tcc ttt ctg aca aac	6588
Arg Thr Asn His Glu Asp Ser Asp Lys Asp His Ser Phe Leu Thr Asn	
2160 2165 2170 2175	
gat gag ctc gct gta ctc cct gtc gtc aaa gtg ctt ccc tct ggt aaa	6636
Asp Glu Leu Ala Val Leu Pro Val Val Lys Val Leu Pro Ser Gly Lys	
2180 2185 2190	
tac acg ggt gcc aac tta aaa tca gtc att cga gtc ctg cgg ggt ttg	6684
Tyr Thr Gly Ala Asn Leu Lys Ser Val Ile Arg Val Leu Arg Gly Leu	
2195 2200 2205	
cta gat caa gga att cct tct aag gag ctg gag aat ctt caa gaa tta	6732
Leu Asp Gln Gly Ile Pro Ser Lys Glu Leu Glu Asn Leu Gln Glu Leu	
2210 2215 2220	
aaa cct ttg gat cag tgt cta att ggg caa act aag gaa aac aga agg	6780
Lys Pro Leu Asp Gln Cys Leu Ile Gly Gln Thr Lys Glu Asn Arg Arg	
2225 2230 2235	
aag aac aga tat aaa aat ata ctt ccc tat gat gct aca aga gtg cct	6828
Lys Asn Arg Tyr Lys Asn Ile Leu Pro Tyr Asp Ala Thr Arg Val Pro	
2240 2245 2250 2255	

ctt gga gat gaa ggt ggc tat atc aat gcc agc ttc att aag ata cca	6876
Leu Gly Asp Glu Gly Gly Tyr Ile Asn Ala Ser Phe Ile Lys Ile Pro	
2260 2265 2270	
gtt ggg aaa gaa gag ttc gtt tac att gcc tgc caa gga cca ctg cct	6924
Val Gly Lys Glu Glu Phe Val Tyr Ile Ala Cys Gln Gly Pro Leu Pro	
2275 2280 2285	
aca act gtt gga gac ttc tgg cag atg att tgg gag caa aaa tcc aca	6972
Thr Thr Val Gly Asp Phe Trp Gln Met Ile Trp Glu Gln Lys Ser Thr	
2290 2295 2300	
gtg ata gcc atg atg act caa gaa gta gaa gga gaa aaa atc aaa tgc	7020
Val Ile Ala Met Met Thr Gln Glu Val Glu Gly Glu Lys Ile Lys Cys	
2305 2310 2315	
cag cgc tat tgg ccc aac atc cta ggc aaa aca aca atg gtc agc aac	7068
Gln Arg Tyr Trp Pro Asn Ile Leu Gly Lys Thr Thr Met Val Ser Asn	
2320 2325 2330 2335	
aga ctt cga ctg gct ctt gtg aga atg cag cag ctg aag ggc ttt gtg	7116
Arg Leu Arg Leu Ala Leu Val Arg Met Gln Gln Leu Lys Gly Phe Val	
2340 2345 2350	
gtg agg gca atg acc ctt gaa gat att cag acc aga gag gtg cgc cat	7164
Val Arg Ala Met Thr Leu Glu Asp Ile Gln Thr Arg Glu Val Arg His	
2355 2360 2365	
att tct cat ctg aat ttc act gcc tgg cca gac cat gat aca cct tct	7212
Ile Ser His Leu Asn Phe Thr Ala Trp Pro Asp His Asp Thr Pro Ser	
2370 2375 2380	
caa cca gat gat ctg ctt act ttt atc tcc tac atg aga cac atc cac	7260
Gln Pro Asp Asp Leu Leu Thr Phe Ile Ser Tyr Met Arg His Ile His	
2385 2390 2395	
aga tca ggc cca atc att acg cac tgc agt gct ggc att gga cgt tca	7308
Arg Ser Gly Pro Ile Ile Thr His Cys Ser Ala Gly Ile Gly Arg Ser	
2400 2405 2410 2415	
ggg acc ctg att tgc ata gat gtg gtt ctg gga tta atc agt cag gat	7356
Gly Thr Leu Ile Cys Ile Asp Val Val Leu Gly Leu Ile Ser Gln Asp	
2420 2425 2430	
ctt gat ttt gac atc tct gat ttg gtg cgc tgc atg aga cta caa aga	7404
Leu Asp Phe Asp Ile Ser Asp Leu Val Arg Cys Met Arg Leu Gln Arg	
2435 2440 2445	
cac gga atg gtt cag aca gag gat caa tat att ttc tgc tat caa gtc	7452
His Gly Met Val Gln Thr Glu Asp Gln Tyr Ile Phe Cys Tyr Gln Val	
2450 2455 2460	
atc ctt tat gtc ctg aca cgt ctt caa gca gaa gaa gag caa aaa cag	7500
Ile Leu Tyr Val Leu Thr Arg Leu Gln Ala Glu Glu Glu Gln Lys Gln	
2465 2470 2475	
cag cct cag ctt ctg aag tga catgaaaaga gcctctggat gcatttccat	7551
Gln Pro Gln Leu Leu Lys	
2480 2485	

ttctctcctt aacctccagc agactcctgc tctctatcca aaataaagat cacagagcag 7611  
 caagttcata caacatgcat gttctcctct atcttagagg ggtattcttc ttgaaaataa 7671  
 aaaatattga aatgctgtat ttttacagct actttaacct atgataatta tttacaaaat 7731  
 ttttaacacta accaaacaat gcagatctta gggatgatta aaggcagcat ttgatgatag 7791  
 cagacattgt tacaaggaca tgggtgagtct atttttaatg caccaatctt gtttatagca 7851  
 aaaatgtttt ccaatatttt aataaagtag ttattttata ggggatactt gaaaccagta 7911  
 ttttaagcttt aaatgacagt aatattggca tagaaaaaag tagcaaatgt ttactgtatc 7971  
 aatttctaata gtttactata tagaatttcc tgtaatatat ttatatactt tttcatgaaa 8031  
 atggagttat cagttatctg tttgttactg catcatctgt ttgtaatcat tatctcactt 8091  
 tgtaaataaaa aacacacctt aaaacatg 8119

<210> 46  
 <211> 2485  
 <212> PRT  
 <213> Homo sapiens

<400> 46

Met	His	Val	Ser	Leu	Ala	Glu	Ala	Leu	Glu	Val	Arg	Gly	Gly	Pro	Leu
1				5					10					15	
Gln	Glu	Glu	Glu	Ile	Trp	Ala	Val	Leu	Asn	Gln	Ser	Ala	Glu	Ser	Leu
			20					25					30		
Gln	Glu	Leu	Phe	Arg	Lys	Val	Ser	Leu	Ala	Asp	Pro	Ala	Ala	Leu	Gly
		35					40					45			
Phe	Ile	Ile	Ser	Pro	Trp	Ser	Leu	Leu	Leu	Leu	Pro	Ser	Gly	Ser	Val
	50					55					60				
Ser	Phe	Thr	Asp	Glu	Asn	Ile	Ser	Asn	Gln	Asp	Leu	Arg	Ala	Phe	Thr
65					70				75					80	
Ala	Pro	Glu	Val	Leu	Gln	Asn	Gln	Ser	Leu	Thr	Ser	Leu	Ser	Asp	Val
				85				90						95	
Glu	Lys	Ile	His	Ile	Tyr	Ser	Leu	Gly	Met	Thr	Leu	Tyr	Trp	Gly	Ala
			100					105					110		
Asp	Tyr	Glu	Val	Pro	Gln	Ser	Gln	Pro	Ile	Lys	Leu	Gly	Asp	His	Leu
	115						120					125			
Asn	Ser	Ile	Leu	Leu	Gly	Met	Cys	Glu	Asp	Val	Ile	Tyr	Ala	Arg	Val
	130					135					140				
Ser	Val	Arg	Thr	Val	Leu	Asp	Ala	Cys	Ser	Ala	His	Ile	Arg	Asn	Ser
145					150				155					160	
Asn	Cys	Ala	Pro	Ser	Phe	Ser	Tyr	Val	Lys	His	Leu	Val	Lys	Leu	Val
				165				170					175		
Leu	Gly	Asn	Leu	Ser	Gly	Thr	Asp	Gln	Leu	Ser	Cys	Asn	Ser	Glu	Gln

180										185										190																																			
Lys	Pro	Asp	Arg	Ser	Gln	Ala	Ile	Arg	Asp	Arg	Leu	Arg	Gly	Lys	Gly																																								
		195					200					205																																											
Leu	Pro	Thr	Gly	Arg	Ser	Ser	Thr	Ser	Asp	Val	Leu	Asp	Ile	Gln	Lys																																								
		210				215					220																																												
Pro	Pro	Leu	Ser	His	Gln	Thr	Phe	Leu	Asn	Lys	Gly	Leu	Ser	Lys	Ser																																								
		225			230					235					240																																								
Met	Gly	Phe	Leu	Ser	Ile	Lys	Asp	Thr	Gln	Asp	Glu	Asn	Tyr	Phe	Lys																																								
				245					250					255																																									
Asp	Ile	Leu	Ser	Asp	Asn	Ser	Gly	Arg	Glu	Asp	Ser	Glu	Asn	Thr	Phe																																								
			260					265						270																																									
Ser	Pro	Tyr	Gln	Phe	Lys	Thr	Ser	Gly	Pro	Glu	Lys	Lys	Pro	Ile	Pro																																								
		275					280						285																																										
Gly	Ile	Asp	Val	Leu	Ser	Lys	Lys	Lys	Ile	Trp	Ala	Ser	Ser	Met	Asp																																								
		290				295					300																																												
Leu	Leu	Cys	Thr	Ala	Asp	Arg	Asp	Phe	Ser	Ser	Gly	Glu	Thr	Ala	Thr																																								
		305			310				315					320																																									
Tyr	Arg	Arg	Cys	His	Pro	Glu	Ala	Val	Thr	Val	Arg	Thr	Ser	Thr	Thr																																								
				325					330					335																																									
Pro	Arg	Lys	Lys	Glu	Ala	Arg	Tyr	Ser	Asp	Gly	Ser	Ile	Ala	Leu	Asp																																								
				340				345					350																																										
Ile	Phe	Gly	Pro	Gln	Lys	Met	Asp	Pro	Ile	Tyr	His	Thr	Arg	Glu	Leu																																								
		355				360						365																																											
Pro	Thr	Ser	Ser	Ala	Ile	Ser	Ser	Ala	Leu	Asp	Arg	Ile	Arg	Glu	Arg																																								
						375					380																																												
Gln	Lys	Lys	Leu	Gln	Val	Leu	Arg	Glu	Ala	Met	Asn	Val	Glu	Glu	Pro																																								
					390					395				400																																									
Val	Arg	Arg	Tyr	Lys	Thr	Tyr	His	Gly	Asp	Val	Phe	Ser	Thr	Ser	Ser																																								
				405					410					415																																									
Glu	Ser	Pro	Ser	Ile	Ile	Ser	Ser	Glu	Ser	Asp	Phe	Arg	Gln	Val	Arg																																								
				420				425					430																																										
Arg	Ser	Glu	Ala	Ser	Lys	Arg	Phe	Glu	Ser	Ser	Ser	Gly	Leu	Pro	Gly																																								
				435			440					445																																											
Val	Asp	Glu	Thr	Leu	Ser	Gln	Gly	Gln	Ser	Gln	Arg	Pro	Ser	Arg	Gln																																								
				450		455					460																																												
Tyr	Glu	Thr	Pro	Phe	Glu	Gly	Asn	Leu	Ile	Asn	Gln	Glu	Ile	Met	Leu																																								
					470				475					480																																									
Lys	Arg	Gln	Glu	Glu	Glu	Leu	Met	Gln	Leu	Gln	Ala	Lys	Met	Ala	Leu																																								
				485				490					495																																										
Arg	Gln	Ser	Arg	Leu	Ser	Leu	Tyr	Pro	Gly	Asp	Thr	Ile	Lys	Ala	Ser																																								

500					505					510						
Met	Leu	Asp	Ile	Thr	Arg	Asp	Pro	Leu	Arg	Glu	Ile	Ala	Leu	Glu	Thr	
515					520					525						
Ala	Met	Thr	Gln	Arg	Lys	Leu	Arg	Asn	Phe	Phe	Gly	Pro	Glu	Phe	Val	
530					535					540						
Lys	Met	Thr	Ile	Glu	Pro	Phe	Ile	Ser	Leu	Asp	Leu	Pro	Arg	Ser	Ile	
545					550					555					560	
Leu	Thr	Lys	Lys	Gly	Lys	Asn	Glu	Asp	Asn	Arg	Arg	Lys	Val	Asn	Ile	
565					570					575						
Met	Leu	Leu	Asn	Gly	Gln	Arg	Leu	Glu	Leu	Thr	Cys	Asp	Thr	Lys	Thr	
580					585					590						
Ile	Cys	Lys	Asp	Val	Phe	Asp	Met	Val	Val	Ala	His	Ile	Gly	Leu	Val	
595					600					605						
Glu	His	His	Leu	Phe	Ala	Leu	Ala	Thr	Leu	Lys	Asp	Asn	Glu	Tyr	Phe	
610					615					620						
Phe	Val	Asp	Pro	Asp	Leu	Lys	Leu	Thr	Lys	Val	Ala	Pro	Glu	Gly	Trp	
625					630					635					640	
Lys	Glu	Glu	Pro	Lys	Lys	Lys	Thr	Lys	Ala	Thr	Val	Asn	Phe	Thr	Leu	
645					650					655						
Phe	Phe	Arg	Ile	Lys	Phe	Phe	Met	Asp	Asp	Val	Ser	Leu	Ile	Gln	His	
660					665					670						
Thr	Leu	Thr	Cys	His	Gln	Tyr	Tyr	Leu	Gln	Leu	Arg	Lys	Asp	Ile	Leu	
675					680					685						
Glu	Glu	Arg	Met	His	Cys	Asp	Asp	Glu	Thr	Ser	Leu	Leu	Leu	Ala	Ser	
690					695					700						
Leu	Ala	Leu	Gln	Ala	Glu	Tyr	Gly	Asp	Tyr	Gln	Pro	Glu	Val	His	Gly	
705					710					715					720	
Val	Ser	Tyr	Phe	Arg	Met	Glu	His	Tyr	Leu	Pro	Ala	Arg	Val	Met	Glu	
725					730					735						
Lys	Leu	Asp	Leu	Ser	Tyr	Ile	Lys	Glu	Glu	Leu	Pro	Lys	Leu	His	Asn	
740					745					750						
Thr	Tyr	Val	Gly	Ala	Ser	Glu	Lys	Glu	Thr	Glu	Leu	Glu	Phe	Leu	Lys	
755					760					765						
Val	Cys	Gln	Arg	Leu	Thr	Glu	Tyr	Gly	Val	His	Phe	His	Arg	Val	His	
770					775					780						
Pro	Glu	Lys	Lys	Ser	Gln	Thr	Gly	Ile	Leu	Leu	Gly	Val	Cys	Ser	Lys	
785					790					795					800	
Gly	Val	Leu	Val	Phe	Glu	Val	His	Asn	Gly	Val	Arg	Thr	Leu	Val	Leu	
805					810					815						
Arg	Phe	Pro	Trp	Arg	Glu	Thr	Lys	Lys	Ile	Ser	Phe	Ser	Lys	Lys	Lys	
820					825					830						

Ile Thr Leu Gln Asn Thr Ser Asp Gly Ile Lys His Gly Phe Gln Thr  
 835 840 845  
 Asp Asn Ser Lys Ile Cys Gln Tyr Leu Leu His Leu Cys Ser Tyr Gln  
 850 855 860  
 His Lys Phe Gln Leu Gln Met Arg Ala Arg Gln Ser Asn Gln Asp Ala  
 865 870 875 880  
 Gln Asp Ile Glu Arg Ala Ser Phe Arg Ser Leu Asn Leu Gln Ala Glu  
 885 890 895  
 Ser Val Arg Gly Phe Asn Met Gly Arg Ala Ile Ser Thr Gly Ser Leu  
 900 905 910  
 Ala Ser Ser Thr Leu Asn Lys Leu Ala Val Arg Pro Leu Ser Val Gln  
 915 920 925  
 Ala Glu Ile Leu Lys Arg Leu Ser Cys Ser Glu Leu Ser Leu Tyr Gln  
 930 935 940  
 Pro Leu Gln Asn Ser Ser Lys Glu Lys Asn Asp Lys Ala Ser Trp Glu  
 945 950 955 960  
 Glu Lys Pro Arg Glu Met Ser Lys Ser Tyr His Asp Leu Ser Gln Ala  
 965 970 975  
 Ser Leu Tyr Pro His Arg Lys Asn Val Ile Val Asn Met Glu Pro Pro  
 980 985 990  
 Pro Gln Thr Val Ala Glu Leu Val Gly Lys Pro Ser His Gln Met Ser  
 995 1000 1005  
 Arg Ser Asp Ala Glu Ser Leu Ala Gly Val Thr Lys Leu Asn Asn Ser  
 1010 1015 1020  
 Lys Ser Val Ala Ser Leu Asn Arg Ser Pro Glu Arg Arg Lys His Glu  
 1025 1030 1035 1040  
 Ser Asp Ser Ser Ser Ile Glu Asp Pro Gly Gln Ala Tyr Val Leu Gly  
 1045 1050 1055  
 Met Thr Met His Ser Ser Gly Asn Ser Ser Ser Gln Val Pro Leu Lys  
 1060 1065 1070  
 Glu Asn Asp Val Leu His Lys Arg Trp Ser Ile Val Ser Ser Pro Glu  
 1075 1080 1085  
 Arg Glu Ile Thr Leu Val Asn Leu Lys Lys Asp Ala Lys Tyr Gly Leu  
 1090 1095 1100  
 Gly Phe Gln Ile Ile Gly Gly Glu Lys Met Gly Arg Leu Asp Leu Gly  
 1105 1110 1115 1120  
 Ile Phe Ile Ser Ser Val Ala Pro Gly Gly Pro Ala Asp Leu Asp Gly  
 1125 1130 1135  
 Cys Leu Lys Pro Gly Asp Arg Leu Ile Ser Val Asn Ser Val Ser Leu  
 1140 1145 1150

Glu Gly Val Ser His His Ala Ala Ile Glu Ile Leu Gln Asn Ala Pro  
 1155 1160 1165  
 Glu Asp Val Thr Leu Val Ile Ser Gln Pro Lys Glu Lys Ile Ser Lys  
 1170 1175 1180  
 Val Pro Ser Thr Pro Val His Leu Thr Asn Glu Met Lys Asn Tyr Met  
 185 1190 1195 1200  
 Lys Lys Ser Ser Tyr Met Gln Asp Ser Ala Ile Asp Ser Ser Ser Lys  
 1205 1210 1215  
 Asp His His Trp Ser Arg Gly Thr Leu Arg His Ile Ser Glu Asn Ser  
 1220 1225 1230  
 Phe Gly Pro Ser Gly Gly Leu Arg Glu Gly Ser Leu Ser Ser Gln Asp  
 1235 1240 1245  
 Ser Arg Thr Glu Ser Ala Ser Leu Ser Gln Ser Gln Val Asn Gly Phe  
 1250 1255 1260  
 Phe Ala Ser His Leu Gly Asp Gln Thr Trp Gln Glu Ser Gln His Gly  
 265 1270 1275 1280  
 Ser Pro Ser Pro Ser Val Ile Ser Lys Ala Thr Glu Lys Glu Thr Phe  
 1285 1290 1295  
 Thr Asp Ser Asn Gln Ser Lys Thr Lys Lys Pro Gly Ile Ser Asp Val  
 1300 1305 1310  
 Thr Asp Tyr Ser Asp Arg Gly Asp Ser Asp Met Asp Glu Ala Thr Tyr  
 1315 1320 1325  
 Ser Ser Ser Gln Asp His Gln Thr Pro Lys Gln Glu Ser Ser Ser Ser  
 1330 1335 1340  
 Val Asn Thr Ser Asn Lys Met Asn Phe Lys Thr Phe Ser Ser Ser Pro  
 345 1350 1355 1360  
 Pro Lys Pro Gly Asp Ile Phe Glu Val Glu Leu Ala Lys Asn Asp Asn  
 1365 1370 1375  
 Ser Leu Gly Ile Ser Val Thr Gly Gly Val Asn Thr Ser Val Arg His  
 1380 1385 1390  
 Gly Gly Ile Tyr Val Lys Ala Val Ile Pro Gln Gly Ala Ala Glu Ser  
 1395 1400 1405  
 Asp Gly Arg Ile His Lys Gly Asp Arg Val Leu Ala Val Asn Gly Val  
 1410 1415 1420  
 Ser Leu Glu Gly Ala Thr His Lys Gln Ala Val Glu Thr Leu Arg Asn  
 425 1430 1435 1440  
 Thr Gly Gln Val Val His Leu Leu Leu Glu Lys Gly Gln Ser Pro Thr  
 1445 1450 1455  
 Ser Lys Glu His Val Pro Val Thr Pro Gln Cys Thr Leu Ser Asp Gln  
 1460 1465 1470  
 Asn Ala Gln Gly Gln Gly Pro Glu Lys Val Lys Lys Thr Thr Gln Val  
 1475 1480 1485

Lys Asp Tyr Ser Phe Val Thr Glu Glu Asn Thr Phe Glu Val Lys Leu  
 1490 1495 1500  
 Phe Lys Asn Ser Ser Gly Leu Gly Phe Ser Phe Ser Arg Glu Asp Asn  
 505 1510 1515 1520  
 Leu Ile Pro Glu Gln Ile Asn Ala Ser Ile Val Arg Val Lys Lys Leu  
 1525 1530 1535  
 Phe Pro Gly Gln Pro Ala Ala Glu Ser Gly Lys Ile Asp Val Gly Asp  
 1540 1545 1550  
 Val Ile Leu Lys Val Asn Gly Ala Ser Leu Lys Gly Leu Ser Gln Gln  
 1555 1560 1565  
 Glu Val Ile Ser Ala Leu Arg Gly Thr Ala Pro Glu Val Phe Leu Leu  
 1570 1575 1580  
 Leu Cys Arg Pro Pro Pro Gly Val Leu Pro Glu Ile Asp Thr Ala Leu  
 585 1590 1595 1600  
 Leu Thr Pro Leu Gln Ser Pro Ala Gln Val Leu Pro Asn Ser Ser Lys  
 1605 1610 1615  
 Asp Ser Ser Gln Pro Ser Cys Val Glu Gln Ser Thr Ser Ser Asp Glu  
 1620 1625 1630  
 Asn Glu Met Ser Asp Lys Ser Lys Lys Gln Cys Lys Ser Pro Ser Arg  
 1635 1640 1645  
 Arg Asp Ser Tyr Ser Asp Ser Ser Gly Ser Gly Glu Asp Asp Leu Val  
 1650 1655 1660  
 Thr Ala Pro Ala Asn Ile Ser Asn Ser Thr Trp Ser Ser Ala Leu His  
 665 1670 1675 1680  
 Gln Thr Leu Ser Asn Met Val Ser Gln Ala Gln Ser His His Glu Ala  
 1685 1690 1695  
 Pro Lys Ser Gln Glu Asp Thr Ile Cys Thr Met Phe Tyr Tyr Pro Gln  
 1700 1705 1710  
 Lys Ile Pro Asn Lys Pro Glu Phe Glu Asp Ser Asn Pro Ser Pro Leu  
 1715 1720 1725  
 Pro Pro Asp Met Ala Pro Gly Gln Ser Tyr Gln Pro Gln Ser Glu Ser  
 1730 1735 1740  
 Ala Ser Ser Ser Ser Met Asp Lys Tyr His Ile His His Ile Ser Glu  
 745 1750 1755 1760  
 Pro Thr Arg Gln Glu Asn Trp Thr Pro Leu Lys Asn Asp Leu Glu Asn  
 1765 1770 1775  
 His Leu Glu Asp Phe Glu Leu Glu Val Glu Leu Leu Ile Thr Leu Ile  
 1780 1785 1790  
 Lys Ser Glu Lys Gly Ser Leu Gly Phe Thr Val Thr Lys Gly Asn Gln  
 1795 1800 1805



Arg Ile Gly Cys Tyr Val His Asp Val Ile Gln Asp Pro Ala Lys Ser  
 1810 1815 1820  
 Asp Gly Arg Leu Lys Pro Gly Asp Arg Leu Ile Lys Val Asn Asp Thr  
 825 1830 1835 1840  
 Asp Val Thr Asn Met Thr His Thr Asp Ala Val Asn Leu Leu Arg Ala  
 1845 1850 1855  
 Ala Ser Lys Thr Val Arg Leu Val Ile Gly Arg Val Leu Glu Leu Pro  
 1860 1865 1870  
 Arg Ile Pro Met Leu Pro His Leu Leu Pro Asp Ile Thr Leu Thr Cys  
 1875 1880 1885  
 Asn Lys Glu Glu Leu Gly Phe Ser Leu Cys Gly Gly His Asp Ser Leu  
 1890 1895 1900  
 Tyr Gln Val Val Tyr Ile Ser Asp Ile Asn Pro Arg Ser Val Ala Ala  
 905 1910 1915 1920  
 Ile Glu Gly Asn Leu Gln Leu Leu Asp Val Ile His Tyr Val Asn Gly  
 1925 1930 1935  
 Val Ser Thr Gln Gly Met Thr Leu Glu Glu Val Asn Arg Ala Leu Asp  
 1940 1945 1950  
 Met Ser Leu Pro Ser Leu Val Leu Lys Ala Thr Arg Asn Asp Leu Pro  
 1955 1960 1965  
 Val Val Pro Ser Ser Lys Arg Ser Ala Val Ser Ala Pro Lys Ser Thr  
 1970 1975 1980  
 Lys Gly Asn Gly Ser Tyr Ser Val Gly Ser Cys Ser Gln Pro Ala Leu  
 985 1990 1995 2000  
 Thr Pro Asn Asp Ser Phe Ser Thr Val Ala Gly Glu Glu Ile Asn Glu  
 2005 2010 2015  
 Ile Ser Tyr Pro Lys Gly Lys Cys Ser Thr Tyr Gln Ile Lys Gly Ser  
 2020 2025 2030  
 Pro Asn Leu Thr Leu Pro Lys Glu Ser Tyr Ile Gln Glu Asp Asp Ile  
 2035 2040 2045  
 Tyr Asp Asp Ser Gln Glu Ala Glu Val Ile Gln Ser Leu Leu Asp Val  
 2050 2055 2060  
 Val Asp Glu Glu Ala Gln Asn Leu Leu Asn Glu Asn Asn Ala Ala Gly  
 065 2070 2075 2080  
 Tyr Ser Cys Gly Pro Gly Thr Leu Lys Met Asn Gly Lys Leu Ser Glu  
 2085 2090 2095  
 Glu Arg Thr Glu Asp Thr Asp Cys Asp Gly Ser Pro Leu Pro Glu Tyr  
 2100 2105 2110  
 Phe Thr Glu Ala Thr Lys Met Asn Gly Cys Glu Glu Tyr Cys Glu Glu  
 2115 2120 2125  
 Lys Val Lys Ser Glu Ser Leu Ile Gln Lys Pro Gln Glu Lys Lys Thr

2130	2135	2140
Asp Asp Asp Glu Ile Thr Trp Gly Asn Asp Glu Leu Pro Ile Glu Arg 145 2150 2155 2160		
Thr Asn His Glu Asp Ser Asp Lys Asp His Ser Phe Leu Thr Asn Asp 2165 2170 2175		
Glu Leu Ala Val Leu Pro Val Val Lys Val Leu Pro Ser Gly Lys Tyr 2180 2185 2190		
Thr Gly Ala Asn Leu Lys Ser Val Ile Arg Val Leu Arg Gly Leu Leu 2195 2200 2205		
Asp Gln Gly Ile Pro Ser Lys Glu Leu Glu Asn Leu Gln Glu Leu Lys 2210 2215 2220		
Pro Leu Asp Gln Cys Leu Ile Gly Gln Thr Lys Glu Asn Arg Arg Lys 225 2230 2235 2240		
Asn Arg Tyr Lys Asn Ile Leu Pro Tyr Asp Ala Thr Arg Val Pro Leu 2245 2250 2255		
Gly Asp Glu Gly Gly Tyr Ile Asn Ala Ser Phe Ile Lys Ile Pro Val 2260 2265 2270		
Gly Lys Glu Glu Phe Val Tyr Ile Ala Cys Gln Gly Pro Leu Pro Thr 2275 2280 2285		
Thr Val Gly Asp Phe Trp Gln Met Ile Trp Glu Gln Lys Ser Thr Val 2290 2295 2300		
Ile Ala Met Met Thr Gln Glu Val Glu Gly Glu Lys Ile Lys Cys Gln 305 2310 2315 2320		
Arg Tyr Trp Pro Asn Ile Leu Gly Lys Thr Thr Met Val Ser Asn Arg 2325 2330 2335		
Leu Arg Leu Ala Leu Val Arg Met Gln Gln Leu Lys Gly Phe Val Val 2340 2345 2350		
Arg Ala Met Thr Leu Glu Asp Ile Gln Thr Arg Glu Val Arg His Ile 2355 2360 2365		
Ser His Leu Asn Phe Thr Ala Trp Pro Asp His Asp Thr Pro Ser Gln 2370 2375 2380		
Pro Asp Asp Leu Leu Thr Phe Ile Ser Tyr Met Arg His Ile His Arg 385 2390 2395 2400		
Ser Gly Pro Ile Ile Thr His Cys Ser Ala Gly Ile Gly Arg Ser Gly 2405 2410 2415		
Thr Leu Ile Cys Ile Asp Val Val Leu Gly Leu Ile Ser Gln Asp Leu 2420 2425 2430		
Asp Phe Asp Ile Ser Asp Leu Val Arg Cys Met Arg Leu Gln Arg His 2435 2440 2445		
Gly Met Val Gln Thr Glu Asp Gln Tyr Ile Phe Cys Tyr Gln Val Ile 2450 2455 2460		

Leu Tyr Val Leu Thr Arg Leu Gln Ala Glu Glu Glu Gln Lys Gln Gln  
 465 2470 2475 2480

Pro Gln Leu Leu Lys  
 2485

<210> 47  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence  
 <400> 47  
 acgtgcatat taccggctgg 20

<210> 48  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence  
 <400> 48  
 gagaaatgat gaagccaagg 20

<210> 49  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence  
 <400> 49  
 gttggctctg aggcacttca 20

<210> 50  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence  
 <400> 50  
 tttgtctctc tcggattcgg 20

<210> 51  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence  
  
 <400> 51  
 gccaaagaaa ttcctcagtt 20  
  
 <210> 52  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 52  
 aaggatgcca gcaataagga 20  
  
 <210> 53  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 53  
 ggtcttcaat ggatgaggag 20  
  
 <210> 54  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 54  
 gtggtgatcc ttggaagaag 20  
  
 <210> 55  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 55  
 tccactccca ctgctgtcac 20  
  
 <210> 56  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

<223> Synthetic Sequence  
 <400> 56  
 ttctctgatt gcctttggtt 20  
  
 <210> 57  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 57  
 gcaactcatc atttcccat 20  
  
 <210> 58  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 58  
 ccagaggctc ttttcatgtc 20  
  
 <210> 59  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 59  
 gcatccagag gctcttttca 20  
  
 <210> 60  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
  
 <400> 60  
 gctggagggtt aaggagagaa 20  
  
 <210> 61  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

<223> Synthetic Sequence  
 <400> 61  
 tttggataga gagcaggagt 20  
  
 <210> 62  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
 <400> 62  
 tttcaagaag aataccccta 20  
  
 <210> 63  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
 <400> 63  
 gctgccttta atcatcccta 20  
  
 <210> 64  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence  
 <400> 64  
 actggtttca agtatcccct 20  
  
 <210> 65  
 <211> 1480  
 <212> DNA  
 <213> Mus musculus  
 <220>  
 <221> CDS  
 <222> (50)..(1033)  
 <300>  
 <303> J. Immunol.  
 <304> 148  
 <306> 1274-1297  
 <307> 1992-02-15  
 <308> M83649/Genbank  
 <309> 1994-04-18  
 <400> 65

gccgcagget gccacacag gccgcccgt gttttccctt gctgcagac atg ctg tgg 58  
 Met Leu Trp  
 1

atc tgg gct gtc ctg cct ctg gtg ctt gct ggc tca cag tta aga gtt 106  
 Ile Trp Ala Val Leu Pro Leu Val Leu Ala Gly Ser Gln Leu Arg Val  
 5 10 15

cat act caa ggt act aat agc atc tcc gag agt tta aag ctg agg agg 154  
 His Thr Gln Gly Thr Asn Ser Ile Ser Glu Ser Leu Lys Leu Arg Arg  
 20 25 30 35

cgg gtt cat gaa act gat aaa aac tgc tca gaa gga tta tat caa gga 202  
 Arg Val His Glu Thr Asp Lys Asn Cys Ser Glu Gly Leu Tyr Gln Gly  
 40 45 50

ggc cca ttt tgc tgt caa cca tgc caa cct ggt aaa aaa aaa gtt gag 250  
 Gly Pro Phe Cys Cys Gln Pro Cys Gln Pro Gly Lys Lys Lys Val Glu  
 55 60 65

gac tgc aaa atg aat ggg ggt aca cca acc tgt gcc cca tgc aca gaa 298  
 Asp Cys Lys Met Asn Gly Gly Thr Pro Thr Cys Ala Pro Cys Thr Glu  
 70 75 80

ggg aag gag tac atg gac aag aac cat tat gct gat aaa tgc aga aga 346  
 Gly Lys Glu Tyr Met Asp Lys Asn His Tyr Ala Asp Lys Cys Arg Arg  
 85 90 95

tgc aca ctc tgc gat gaa gag cat ggt tta gaa gtg gaa aca aac tgc 394  
 Cys Thr Leu Cys Asp Glu Glu His Gly Leu Glu Val Glu Thr Asn Cys  
 100 105 110 115

acc ctg acc cag aat acc aag tgc aag tgc aaa cca gac ttc tac tgc 442  
 Thr Leu Thr Gln Asn Thr Lys Cys Lys Cys Lys Pro Asp Phe Tyr Cys  
 120 125 130

gat tct cct ggc tgt gaa cac tgt gtt cgc tgc gcc tcg tgt gaa cat 490  
 Asp Ser Pro Gly Cys Glu His Cys Val Arg Cys Ala Ser Cys Glu His  
 135 140 145

gga acc ctt gag cca tgc aca gca acc agc aat aca aac tgc agg aaa 538  
 Gly Thr Leu Glu Pro Cys Thr Ala Thr Ser Asn Thr Asn Cys Arg Lys  
 150 155 160

caa agt ccc aga aat cgc cta tgg ttg ttg acc atc ctt gtt ttg tta 586  
 Gln Ser Pro Arg Asn Arg Leu Trp Leu Leu Thr Ile Leu Val Leu Leu  
 165 170 175

att cca ctt gta ttt ata tat cga aag tac cgg aaa aga aag tgc tgg 634  
 Ile Pro Leu Val Phe Ile Tyr Arg Lys Tyr Arg Lys Arg Lys Cys Trp  
 180 185 190 195

aaa agg aga cag gat gac cct gaa tct aga acc tcc agt cgt gaa acc 682  
 Lys Arg Arg Gln Asp Asp Pro Glu Ser Arg Thr Ser Ser Arg Glu Thr  
 200 205 210

ata cca atg aat gcc tca aat ctt agc ttg agt aaa tac atc ccg aga 730  
 Ile Pro Met Asn Ala Ser Asn Leu Ser Leu Ser Lys Tyr Ile Pro Arg  
 215 220 225

att gct gaa gac atg aca atc cag gaa gct aaa aaa ttt gct cga gaa 778  
 Ile Ala Glu Asp Met Thr Ile Gln Glu Ala Lys Lys Phe Ala Arg Glu  
 230 235 240

aat aac atc aag gag ggc aag ata gat gag atc atg cat gac agc atc 826  
 Asn Asn Ile Lys Glu Gly Lys Ile Asp Glu Ile Met His Asp Ser Ile  
 245 250 255

caa gac aca gct gag cag aaa gtc cag ctg ctc ctg tgc tgg tac caa 874  
 Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Leu Cys Trp Tyr Gln  
 260 265 270 275

tct cat ggg aag agt gat gca tat caa gat tta atc aag ggt ctc aaa 922  
 Ser His Gly Lys Ser Asp Ala Tyr Gln Asp Leu Ile Lys Gly Leu Lys  
 280 285 290

aaa gcc gaa tgt cgc aga acc tta gat aaa ttt cag gac atg gtc cag 970  
 Lys Ala Glu Cys Arg Arg Thr Leu Asp Lys Phe Gln Asp Met Val Gln  
 295 300 305

aag gac ctt gga aaa tca acc cca gac act gga aat gaa aat gaa gga 1018  
 Lys Asp Leu Gly Lys Ser Thr Pro Asp Thr Gly Asn Glu Asn Glu Gly  
 310 315 320

caa tgt ctg gag tga aaactacctc agttccagcc atgaagagag gagagagcct 1073  
 Gln Cys Leu Glu  
 325

gccacccatg atggaaacaa aatgaatgcc aactgtattg acattggcaa ctcttggtgt 1133  
 gttctctttg ccagcaaattg gtagttgata ctgagtgagg gtcaaattgac tagcagggttc 1193  
 cagggactgc ttctgttatt ctctgcagtt gctgagatga accattttct ctgtctactg 1253  
 caattttttac attcaaattgt ccatgaaatt tgtattaaat gtgaagtgga atctgcagtg 1313  
 tttgtgttta tattcatata ctatgaactg aggagaatta taaactgaaa caaatactcg 1373  
 cagttaattg aagaccttcc attgatggac agttcttttc ctctctatat ggaaatgtat 1433  
 aatagaagaa ataattttta aattaaagta tctctttttg catttca 1480

<210> 66  
 <211> 327  
 <212> PRT  
 <213> Mus musculus

<400> 66  
 Met Leu Trp Ile Trp Ala Val Leu Pro Leu Val Leu Ala Gly Ser Gln  
 1 5 10 15  
 Leu Arg Val His Thr Gln Gly Thr Asn Ser Ile Ser Glu Ser Leu Lys  
 20 25 30  
 Leu Arg Arg Arg Val His Glu Thr Asp Lys Asn Cys Ser Glu Gly Leu  
 35 40 45  
 Tyr Gln Gly Gly Pro Phe Cys Cys Gln Pro Cys Gln Pro Gly Lys Lys  
 50 55 60



Lys Val Glu Asp Cys Lys Met Asn Gly Gly Thr Pro Thr Cys Ala Pro  
 65 70 75 80  
 Cys Thr Glu Gly Lys Glu Tyr Met Asp Lys Asn His Tyr Ala Asp Lys  
 85 90 95  
 Cys Arg Arg Cys Thr Leu Cys Asp Glu Glu His Gly Leu Glu Val Glu  
 100 105 110  
 Thr Asn Cys Thr Leu Thr Gln Asn Thr Lys Cys Lys Cys Lys Pro Asp  
 115 120 125  
 Phe Tyr Cys Asp Ser Pro Gly Cys Glu His Cys Val Arg Cys Ala Ser  
 130 135 140  
 Cys Glu His Gly Thr Leu Glu Pro Cys Thr Ala Thr Ser Asn Thr Asn  
 145 150 155 160  
 Cys Arg Lys Gln Ser Pro Arg Asn Arg Leu Trp Leu Leu Thr Ile Leu  
 165 170 175  
 Val Leu Leu Ile Pro Leu Val Phe Ile Tyr Arg Lys Tyr Arg Lys Arg  
 180 185 190  
 Lys Cys Trp Lys Arg Arg Gln Asp Asp Pro Glu Ser Arg Thr Ser Ser  
 195 200 205  
 Arg Glu Thr Ile Pro Met Asn Ala Ser Asn Leu Ser Leu Ser Lys Tyr  
 210 215 220  
 Ile Pro Arg Ile Ala Glu Asp Met Thr Ile Gln Glu Ala Lys Lys Phe  
 225 230 235 240  
 Ala Arg Glu Asn Asn Ile Lys Glu Gly Lys Ile Asp Glu Ile Met His  
 245 250 255  
 Asp Ser Ile Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Leu Cys  
 260 265 270  
 Trp Tyr Gln Ser His Gly Lys Ser Asp Ala Tyr Gln Asp Leu Ile Lys  
 275 280 285  
 Gly Leu Lys Lys Ala Glu Cys Arg Arg Thr Leu Asp Lys Phe Gln Asp  
 290 295 300  
 Met Val Gln Lys Asp Leu Gly Lys Ser Thr Pro Asp Thr Gly Asn Glu  
 305 310 315 320  
 Asn Glu Gly Gln Cys Leu Glu  
 325

<210> 67  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Sequence

<400> 67  
 gcagcaaggg aaaacagcgg 20

<210> 68  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 68  
 ccacagcatg tctgcagcaa 20

<210> 69  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 69  
 tttcatgaac ccgcctcctc 20

<210> 70  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 70  
 gggtcagggt gcagtttggt 20

<210> 71  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 71  
 gaggcgcagc gaacacagtg 20

<210> 72  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 72  
 cataggcgat ttctgggact 20

<210> 73  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 73  
 tccagcactt tcttttccgg 20

<210> 74  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 74  
 ggtttcacga ctggaggttc 20

<210> 75  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 75  
 cttcagcaat tctcgggatg 20

<210> 76  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 76  
 gccctccttg atgttatattt 20

<210> 77  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 77  
 ggtaccagca caggagcagc 20

<210> 78  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 78  
 cggctttttt gagacccttg 20

<210> 79  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 79  
 gtgtctgggg ttgattttcc 20

<210> 80  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 80  
 tctcctctct tcatggctgg 20

<210> 81  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 81  
 ggcattcatt ttgtttccat 20

<210> 82  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic Sequence

<400> 82  
 tccctggaac ctgctagtca 20

<210> 83  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 83  
 tcagcaactg cagagaataa 20

<210> 84  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 84  
 gcagattcca cttcacattt 20

<210> 85  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 85  
 aaggtcttca attaactgcg 20

<210> 86  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 86  
 tccgtcatcg ctccctcaggg 20

<210> 87  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 87

atgcattctg cccccaagga

20

<210> 88

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 88

tcatgacact aagtcaagtt aaaggcttt

29

<210> 89

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 89

tcttggacat tgtcattctt gatctc

26

<210> 90

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Probe

<400> 90

attttggctt cattgacacc attctttcga a

31

<210> 91

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 91

caacggattt ggtcgtattg g

21

<210> 92

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 92

ggcaacaata tccactttac cagagt

26

<210> 93  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR Probe

<400> 93  
 cgcttggtca ccagggctgc t

21

<210> 94  
 <211> 2165  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1782) ... (1813)

<400> 94  
 aagctttttt ggctacattt ttttatttgt aaagtaagtt taataatcac tcatctcact 60  
 gggctataat gataagtatt aagtaaggaa gatccacata tgtgagttgc tggcttataa 120  
 ttcacactca agagatactg attttgtcaa ttgtcctttc cccttttttt ctctcttccc 180  
 tccttccatt ccttcttccc ttacctctcc ttctcttccc tcacaccctt tttccttcc 240  
 tctttttaca tttttttatt taaatgaact tttcattttg gaatagtttt aggatttcaa 300  
 aaaatttgca gagataatac agagaatgcc catataccat cctccttata ccacttcttt 360  
 ttgtgtctat tagatgctca gagtgtgtgc acaaggctgg cacaccaggt gtcttctca 420  
 tggcactaac agtctactga aagggtggaac agagacaagc ctatcaacac ctacaagact 480  
 ggtggttaagt gcagtgcag atgcaaaaca caggggtgatg gaaagccctc aggagggtaa 540  
 cctaacctag atttgagggc ccaaacaggc tccagaagaa aatgtcaact gagaggaagc 600  
 ctgaaggatg aacagtgggc taagcaaagg gttattaatg tgttattaat gggttgaatc 660  
 taattgggaa gggagagagg ttgcagagtg aggtgcagag cttggtggac gatgccaaag 720  
 gaatactgaa acctttagtg tgtccagtct ggaactgcat ccaaattcag gttcagtaat 780  
 gatgtcatta tccaaacata ctttctgtaa aattcatgct aaactaccta agagctatct 840  
 accgttccaa agcaatagtg actttgaaca gtgttcacca gagcacgaaa gaattacaag 900  
 attttttttt aaagaaaatt ggccaggaaa taatgagtaa cgaaggacag gaagtaattg 960  
 tgaatgttta atatagctgg ggctatgcga tttggcttaa gttgttagct ttgttttcc 1020  
 cttgagaaat aaaaactaag gggccctccc ttttcagagc cctatggcgc aacatctgta 1080

```

ctttttcata tggttaactg tccattccag gaacgtctgt gagcctctca tgttgagacc 1140
acaacatgga cagcccagtc aaatgccccg caagtctttc tctgagtgac tccagcaatt 1200
agccaaggct cctgtaccca ggcaggacct ctgcgctctg agctccattc tccttcaaga 1260
cctccccaac ttcccagggt gaactacagc agaagccttt agaaagggca ggaggccggc 1320
tctcgaggtc ctacactgaa gtgagcatgc cagccactgc aggaacgccc cgggacagga 1380
atgcccattt gtgcaacgaa ccctgactcc ttctcacc ccctccctac 1440
ccgcgcgcag gccaagttgc tgaatcaatg gagccctccc caaccgggc gttccccagc 1500
gaggcttctt tcccatctc ctgaccaccg gggcttttcg tgagctcgtc tctgatctcg 1560
cgcaagagtg acacacaggt gttcaaagac gcttctgggg agtgaggga gcggtttacg 1620
agtgacttgg ctggagcctc aggggcgggc actggcacgg aacacaccct gaggccagcc 1680
ctggctgccc aggcggagct gcctcttctc ccgcgggttg gtggaccgc tcagtacgga 1740
gttggggaag ctctttcact tcggaggatt gctcaacaac c atg ctg ggc atc tgg 1796
                                   Met Leu Gly Ile Trp
                                   1       5

```

```

acc ctc cta cct ctg gt gagccctctc ctgcccgggt ggaggcttac ccgctcttag 1853
Thr Leu Leu Pro Leu
                                   10

```

```

tcccggggat aggcaaagtg gggcgggcgc gggacgcgtg cgggattgcg gcggcagcgg 1913
cgcacgcggg cacctgggag cggcgggctg ctgcccggag cgttggagac tggctcccg 1973
gggctgttag gaccttcctt caggcccggg tgctcagaac gctggaggac ttgcttttct 2033
tgggccttga tgcgaagtgc tgaccccgct gggcaggcgg ggcagctccg gcgctcctcg 2093
gagaccactg cgctccacgt tgaggtgggc gtggggggcg gacaggaatt gaagcgggaag 2153
tctgggaagc tt 2165

```

```

<210> 95
<211> 623
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (155)...(320)

```

```

<400> 95
ctttcttgga gagagaaatc tgaaagacag tggagccctc acattgtctt tgctgtgca 60
cagcagatac tgccaatttt ggggtgggtta cactgggtta cacgttgctt acttcagaaa 120
tcaataaaat tctcttcatg cttttatttt acag gtt ctt acg tct gtt gct aga 175
                                   Val Leu Thr Ser Val Ala Arg
                                   1       i       5

```



```

tta tcg tcc aaa agt gtt aat gcc caa gtg act gac atc aac tcc aag      223
Leu Ser Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser Lys
      10              15              20

gga ttg gaa ttg agg aag act gtt act aca gtt gag act cag aac ttg      271
Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn Leu
      25              30              35

gaa ggc ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct cca      319
Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro
      40              45              50              55

g gtatgttaca caaaacatcc agagattaca gtgaaagtca cagttaggag tagcacatag 380

taatcatgac tataataatt ttacagtttt tggttccctt atattatata acataactga 440

gagaaaaaca actatgaaat tattttccaa agatgagttt tatttatatt tatcatgctt 500

at ttgatgtg gttatggata aatttaattt acaagtgaca tgcacctctg aaatgagaag 560

actggtctat ttgggtccat ttttttctaa gcaaaaatga ctcat ttgtg aatatgaaag 620

ctt 623

<210> 96
<211> 924
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (146)...(283)

<400> 96
ccccattgt atttatatct cattagccta cccccctcc ccttgtgttt tagaagagtt      60

ttattgtctg tcatccctct atacttccca ccctgttacc tgcccgtgtc ctgttcaaac      120

acttgctcct tttttccttg ggcag gtg aaa gga aag cta ggg act gca cag      172
          Val Lys Gly Lys Leu Gly Thr Ala Gln
          1              5

tca atg ggg atg aac cag act gcg tgc cct gcc aag aag gga agg agt      220
Ser Met Gly Met Asn Gln Thr Ala Cys Pro Ala Lys Lys Gly Arg Ser
      10              15              20              25

aca cag aca aag ccc att ttt ctt cca aat gca gaa gat gta gat tgt      268
Thr Gln Thr Lys Pro Ile Phe Leu Pro Asn Ala Glu Asp Val Asp Cys
          30              35              40

gtg atg aag gac atg gtaagagtct taaaatgcaa ttgaaagagg ccaatcttgg      323
Val Met Lys Asp Met
          45

aatttcatgt agaaccattt ataagacaat ttgaaattgg ggcctactgt ggtgctatgt      383

tgacacacag gaaaggggaag gacaggtggc taggggtaccg cagaaccagg tgccgagcta      443

```



<222> (766)...(828)

<400> 98

```
aactcagaca acctgattgt gaatgtttgt ctgtctgaag gaaatcacac atgaacctet    60
tgagtctcct gatcaccacc ggttgctaaa agtggcagcc tctaagggca gctgagtacc    120

ctccctgagc tacatcatgg gcgtggctat cacctggcca ttttcttggt ctataggaat    180
tttttgaaat tacttttgac agtttatttt aagagctagt ttaagctata ggatttacgt    240
gttcagttta ttactagggt taagtttatt tttgtatcca cttcatctct cttgtgtgtc    300
actattttcc tatcttcctt taactcttga aatcttaaga cagtcattcc ttatgatatt    360
tttcatccag ccatccaaat tatattaact tgtgccagct ttagatacta atttagaaat    420
atttgaagga atacgtttgc cagagatgca aagatgaata aaatggcccc taatttacia    480
agtgccattg aaaattataa aggaattatt ctgccaggct tttgaatttc tcctgtattt    540
ttttttctag  atg tgt aca tgg aat cat caa gga atg cac act cac cag    589
               Met Cys Thr Trp Asn His Gln Gly Met His Thr His Gln
                 1             5             10

caa cac caa gtg caa aga gga agg taattatttt tttacgggta tattctcctt    643
Gln His Gln Val Gln Arg Gly Arg
   15             20

tcccccaacc ccatggaaag atgtgaagaa aaaccaatca ctcttgatta gtagaaagtc    703
ctttatttaa tcttaaagat tgcttatttt catataaaat gtccaatggt ccaacctaca    763

gg atc cag atc tat ctt ggg gtg gct ttg tct tct tct ttt gcc aat    810
  Ile Gln Ile Tyr Leu Gly Val Ala Leu Ser Ser Ser Phe Ala Asn
        25             30             35

tcc act aat tgt ttg ggg taagttcttg ctttgttcaa actgcag    855
Ser Thr Asn Cys Leu Gly
      40
```

<210> 99

<211> 338

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (79)...(161)

<400> 99

```
tcttagtggt aaagtatggt ctcacatgca ttctacaagg ctgagacctg agttgataaa    60

atctctttgt tctttcag tga aga gaa agg aag tac aga aaa cat gca gaa    111
               Arg Glu Arg Lys Tyr Arg Lys His Ala Glu
                 1             5             10

agc aca gaa agg aaa acc aag gtt ctc atg aat ctc caa cct tat atc    159
Ser Thr Glu Arg Lys Thr Lys Val Leu Met Asn Leu Gln Pro Tyr Ile
   15             20             25
```

ct gtaggtattg aaataggtat cagctttcct tgaaaagaaa aatagagaaa 211  
 ttagtgattt ggctttttgt tacttccttt tacttttttg tttcttggtt gtttcatttt 271  
 gtttgagatg gagtcttgct ccatagccca ggctggagtg caggggtgca atcatggctc 331  
 actgcag 338

<210> 100  
 <211> 734  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (255)...(279)

<400> 100  
 gaattcttta gggtttcttgc ctttaaaaac taagacaata ttgcttagtt tctggcaagg 60  
 ccggaacctt tcagaataaa aattgaatgg taaaagtaac cttcttaatc acttaatcta 120  
 gcttcctaata tttatacatc aagcaactga ttgtacttct ttctgaatta aggaaaaatt 180  
 agaagttcac atttagaata ttctaaagat atatttttat ttgtctttct ctgcttccat 240  
 tttttgcttt ctag gaa aca gtg gca ata aat tta tot g gtaaggcttt 289  
                   Glu Thr Val Ala Ile Asn Leu Ser  
                   1                  5  
 tatcatttta tttcatagag atggcatcct ttagagtaat aggccaattt cagagtaaaa 349  
 taatgttact aatttcagtg acatattatg ggatcttggtt atttctcata cattctacct 409  
 gctcagcata aagcatttat caggcagttt gtttaaattt ataatgagta ctcatagtta 469  
 aaaataatca agtaacaata agacacaata gtctgaggct taagaaactt ttccttcata 529  
 atcagctaga tgtattacag aactcctgcc taaaaagatc tagagggttaa agtgtactgt 589  
 agactcaggt attatcagtg taccctaactc tataacaaca tacatgattc cattcagtgg 649  
 ttctttgatc tgtgatttag agataagatg atcataaact ctttgcttat accttttagat 709  
 ttgtgggtca ttgatcattg gatcc 734

<210> 101  
 <211> 1840  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (95)...(426)

<400> 101  
 ttctgaagta ctataaaaga gaaataaaca tggttttcac taatgggaat ttcatttaga 60

aaaacaaatt ttcagactat tttctatttt tcag atg ttg act tgt gta aat ata	115
Met Leu Thr Cys Val Asn Ile	
1 5	
tca cca cta ttg ctg gag tca tgt cac tat gtc aag tta aag gct ttg	163
Ser Pro Leu Leu Leu Glu Ser Cys His Tyr Val Lys Leu Lys Ala Leu	
10 15 20	
ttc gaa aga atg gtg tca atg aag cca aaa tag atg aga tca aga atg	211
Phe Glu Arg Met Val Ser Met Lys Pro Lys Met Arg Ser Arg Met	
25 30 35	
aca atg tcc aag aca cag cag aac aga aag ttc aac tgc ttc gta att	259
Thr Met Ser Lys Thr Gln Gln Asn Arg Lys Phe Asn Cys Phe Val Ile	
40 45 50 55	
ggc atc aac ttc atg gaa aga aag aag cgt atg aca cat tga tta aag	307
Gly Ile Asn Phe Met Glu Arg Lys Lys Arg Met Thr His Leu Lys	
60 65 70	
atc tca aaa aag cca atc ttt gta ctc ttg cag aga aaa ttc aga cta	355
Ile Ser Lys Lys Pro Ile Phe Val Leu Leu Gln Arg Lys Phe Arg Leu	
75 80 85	
tca tcc tca agg aca tta cta gtg act cag aaa att caa act tca gaa	403
Ser Ser Ser Arg Thr Leu Leu Val Thr Gln Lys Ile Gln Thr Ser Glu	
90 95 100	
atg aaa tcc aaa gct tgg tct ag agtgaaaaac aacaaattca gttctgagta	456
Met Lys Ser Lys Ala Trp Ser	
105 110	
tatgcaatta gtgtttgaaa agattcttaa tagctggctg taaatactgc ttggtttttt	516
actgggtaca ttttatcatt tattagcgct gaagagccaa catatttgta gatttttaaat	576
atctcatgat tctgectcca aggatgttta aaatctagtt gggaaaacaa acttcatcaa	636
gagtaaatgc agtggcatgc taagtaccca aataggagtg tatgcagagg atgaaagatt	696
aagattatgc tctggcatct aacatatgat tctgtagtat gaatgtaatc agtgtatggt	756
agtacaaatg tctateccaca ggctaacccc actctatgaa tcaatagaag aagctatgac	816
cttttgctga aatatcagtt actgaacagg caggccactt tgcctctaaa ttacctctga	876
taattctaga gattttacca tattttctaaa ctttgtttat aactctgaga agatcatatt	936
tatgtaaagt atatgtattt gagtgcagaa tttaaataag gctctacctc aaagaccttt	996
gcacagttta ttgggtgcat attatacaat atttcaattg tgaattcaca tagaaaacat	1056
taaattataa tgtttgacta ttatatatgt gtatgcattt tactgggtca aaactaccta	1116
cttctttctc aggcatacaa agcattttga gcaggagagt attactagag ctttgccacc	1176
tctccatttt tgccttggtg ctcatcttaa tggcctaattg ccccccaaa catggaaata	1236
tcaccaaaaa atacttaata gtccacaaaa aggcaagact gcccttagaa attctagcct	1296

ggtttggaga tactaactgc tctcagagaa agtagctttg tgacatgtca tgaacccatg 1356  
 tttgcaatca aagatgataa aatagattct ttttttccc ccacccccga aaatgttcaa 1416  
 taatgtccca tgtaaaacct gctacaaatg gcagcttata catagcaatg gtaaaatcat 1476  
 catctggatt taggaattgc tcttgtcata cccccaagtt tctaagattt aagattctcc 1536  
 ttactactat cctacgttta aatatctttg aaagtttgta ttaaagtga attttaagaa 1596  
 ataataattta ttttctgta aatgtaaact gtgaagatag ttataaactg aagcagatac 1656  
 ctggaaccac ctaaagaact tccatttatg gaggattttt ttgccccttg tgtttggaat 1716  
 tataaaatat aggtaaaagt acgtaattaa ataatgtttt tggattttct ggttttctct 1776  
 tttttggtag gggcttgctt tttgggtttg tcttcctttt ctctaactga tgctaaatat 1836  
 aact 1840

<210> 102  
 <211> 836  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(399)

<400> 102  
 atg ctg ggc atc tgg acc ctc cta cct ctg gtt ctt acg tct gtt gct 48  
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala  
 1 5 10 15  
 aga tta tcg tcc aaa agt gtt aat gcc caa gtg act gac atc aac tcc 96  
 Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser  
 20 25 30  
 aag gga ttg gaa ttg agg aag act gtt act aca gtt gag act cag aac 144  
 Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn  
 35 40 45  
 ttg gaa ggc ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct 192  
 Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
 50 55 60  
 cca ggt gaa agg aaa gct agg gac tgc aca gtc aat ggg gat gaa cca 240  
 Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
 65 70 75 80  
 gac tgc gtg ccc tgc caa gaa ggg aag gag tac aca gac aaa gcc cat 288  
 Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
 85 90 95  
 ttt tct tcc aaa tgc aga aga tgt aga ttg tgt gat gaa gga cat gat 336  
 Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Asp  
 100 105 110  
 gtg aac atg gaa tca tca agg aat gca cac tca cca gca aca cca agt 384  
 Val Asn Met Glu Ser Ser Arg Asn Ala His Ser Pro Ala Thr Pro Ser  
 115 120 125

gca aag agg aag tga agagaaagga agtacagaaa acatgcagaa agcacagaaa 439  
 Ala Lys Arg Lys  
 130

ggaaaaccaa gggttctcatg aatctccaac cttaaattcct gaaacagtgg caataaattt 499  
 atctgatgtt gacttgagta aatatatcac cactattgct ggagtcatga cactaagtca 559  
 agttaaaggc tttgttcgaa agaattgggtgt caatgaagcc aaaatagatg agatcaagaa 619  
 tgacaatgtc caagacacag cagaacagaa agttcaactg cttcgttaatt ggcatcaact 679  
 tcatggaaag aaagaagcgt atgacacatt gattaaagat ctcaaaaaag ccaatctttg 739  
 tactcttgca gagaaaattc agactatcat cctcaaggac attactagtg actcagaaaa 799  
 ttcaaacttc agaaatgaaa tccaaagctt ggtctag 836

<210> 103  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 103  
 tgaggaagga gtcagggttc 20

<210> 104  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 104  
 ggtggtcagg aggatgggaa 20

<210> 105  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 105  
 agccagtctc caacgcctcc 20

<210> 106  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 106  
tgccccgcct gccacgagg

20

<210> 107  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 107  
acacctgtgt gtcactcttg

20

<210> 108  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 108  
gccaaagtcac tcgtaaaccg

20

<210> 109  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 109  
aatcctccga agtgaaagag

20

<210> 110  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 110  
atgccagca tggttgttga

20

<210> 111  
<211> 20  
<212> DNA  
<213> Artificial Sequence



<220>  
 <223> Antisense Oligonucleotide  
  
 <400> 111  
 acgtaagaac cagaggtagg 20  
  
 <210> 112  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 112  
 ttttgacga taatctagca 20  
  
 <210>113  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 113  
 ttcctttcac ctggaggaca 20  
  
 <210> 114  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 114  
 cagtccctag ctttcctttc 20  
  
 <210> 115  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 115  
 agccatgtcc ttcacacac 20  
  
 <210> 116  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide  
  
 <400> 116  
 gggtcacagt gttcacatac 20  
  
 <210> 117  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 117  
 gttgctggtg agtgtgcatt 20  
  
 <210> 118  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 118  
 acttcctttc tcttcaccca 20  
  
 <210> 119  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 119  
 tggttttcct ttctgtgctt 20  
  
 <210> 120  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 120  
 tttaagggtg gagattcatg 20  
  
 <210> 121  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide  
  
 <400> 121  
 gatttaaggt tggagattca 20  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 122  
 ccactgtttc aggatttaag 20  
  
 <210> 123  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 123  
 gtcaacatca gataaattta 20  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 124  
 ttactcaag tcaacatcag 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 125  
 ttagtgtcat gactccagca 20  
  
 <210> 126  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Antisense Oligonucleotide  
 <400> 126  
 aacttgactt agtgtcatga 20  
 <210> 127  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide  
 <400> 127  
 tacgaagcag ttgaactttc 20  
 <210> 128  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide  
 <400> 128  
 ttgagatctt taatcaatgt 20  
 <210> 129  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide  
 <400> 129  
 gtccttgagg atgatagtct 20  
 <210> 130  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide  
 <400> 130  
 ttggatttca tttctgaagt 20  
 <210> 131  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide

<400> 131  
tttttctctc tagaccaagc 20

<210> 132  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Antisense Oligonucleotide

<400> 132  
aagcagtatt tacagccagc 20

<210> 133  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Antisense Oligonucleotide

<400> 133  
tcagcgctaa taaatgataa 20

<210> 134  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Antisense Oligonucleotide  
<400> 134  
ctcttcagcg ctaataaatg 20

<210> 135  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Antisense Oligonucleotide

<400> 135  
atgccactgc atttactctt 20

<210> 136  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 136  
 catgccactg catttactct 20

<210> 137  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 137  
 acattcatatc tacagaatca 20

<210> 138  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 138  
 catacactga ttacattcat 20

<210> 139  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 139  
 ttacataaat atgatcttct 20

<210> 140  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 140  
 gaggtagagc cttattttaa 20

<210> 141  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 141  
 gtataatatg acaccaataa 20

<210> 142  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide

<400> 142  
 aatattgtat aatatgacac 20

<210> 143  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide

<400> 143  
 gtgaattcac aattgaaata 20

<210> 144  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide

<400> 144  
 attataattt aatgttttct 20

<210> 145  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide

<400> 145  
 tactctcctg ctcaaaatgc 20

<210> 146  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide

<400> 146

tggtggacta ttaagtattt

20

<210> 147

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 147

agagcagtta gtatctccaa

20

<210> 148

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 148

caaagctact ttctctgaga

20

<210> 149

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 149

gacatgtcac aaagctactt

20

<210> 150

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 150

ttatcatctt tgattgcaaa

20

<210> 151

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 151



atgggacatt attgaacatt 20

<210> 152  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 152  
 attcacatth aatacaaact 20

<210> 153  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 153  
 atataaatat tattttcttaa 20

<210> 154  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 154  
 ctatgtgcta ctctaactg 20

<210> 155  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 155  
 tgattactat gtgctactcc 20

<210> 156  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense Oligonucleotide

<400> 156  
 tataaataaaa actcatcttt 20

<210> 157  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 157  
 cttccctttc ctgtgtgtca 20

<210> 158  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 158  
 taccctagcc acctgtcctt 20

<210> 159  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 159  
 ctggaagaat tgcctagact 20

<210> 160  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 160  
 atatttactc attctcctat 20

<210> 161  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 161  
 atgtccagag gtttcttcat 20

<210> 162  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 162  
 agaaacattg ctttataggc 20

<210> 163  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 163  
 atgacaccag taatacagtc 20

<210> 164  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 164  
 tttgagatcc actgcttata 20

<210> 165  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
 <400> 165  
 gtttggaac tattagttat 20

<210> 166  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 166  
 atgtgtgatt tccttcagac 20

<210> 167  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 167  
 atcataagga atgactgtct 20  
  
 <210> 168  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 168  
 aatggcactt tgtaaattag 20  
  
 <210> 169  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 169  
 tataattttc aatggcactt 20  
  
 <210> 170  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 170  
 cagaataatt cctttataat 20  
  
 <210> 171  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 171  
 ccatgttcac atctagaaaa 20

<210> 172  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 172  
 tctcttcact gaaagaacaa 20  
  
 <210> 173  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 173  
 aggaaagctg atacctatatt 20  
  
 <210> 174  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 174  
 catctctatg aaataaaatg 20  
  
 <210> 175  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 175  
 ggaaaagttt cttaagcctc 20  
  
 <210> 176  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense Oligonucleotide  
  
 <400> 176  
 ttatctctaa atcacagatc 20  
  
 <210> 177

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 177  
aaagagaaaa ccagaaatac 20

<210> 178  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 178  
gttagagaaa aggaagacaa 20

<210> 179  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 179  
atgttcacat catgtccttc 20

<210> 180  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Antisense Oligonucleotide

<400> 180  
tcgatctcct tttatgcccg 20